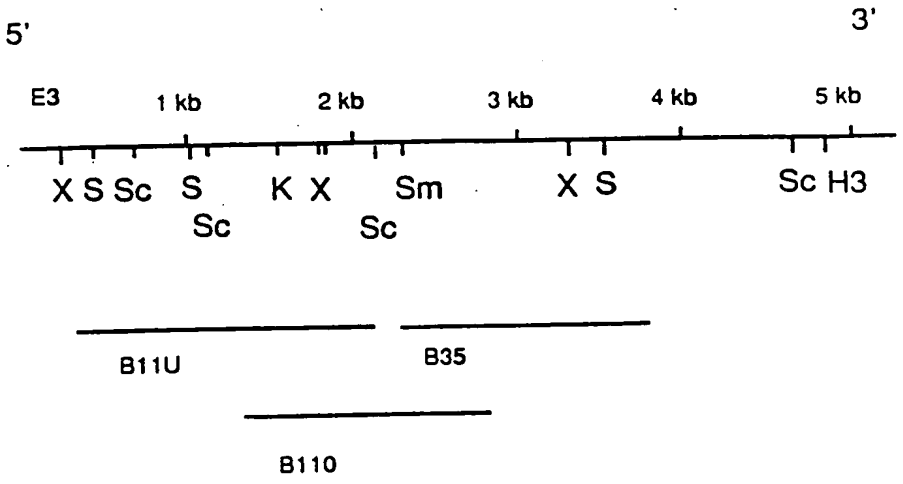
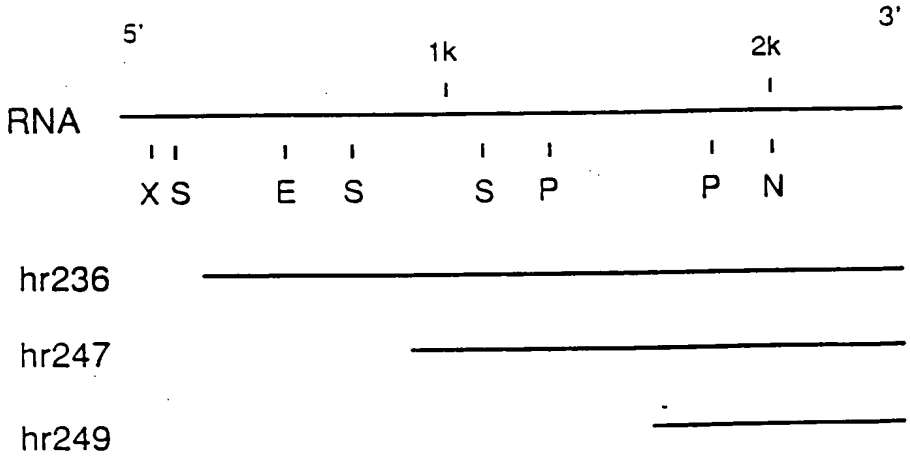
Map of HaSV RNA 1 clones



H3=Hind3, K=Kpn1, Sc=Sac1, S=Sal1, Sm=Sma1, X=Xho1

FIG. 1a

Map of HaSV RNA 2 clones



E=EcoR1, N=Not1, P=Pst1, S=Sal1, X=Xho1

FIG. 1b

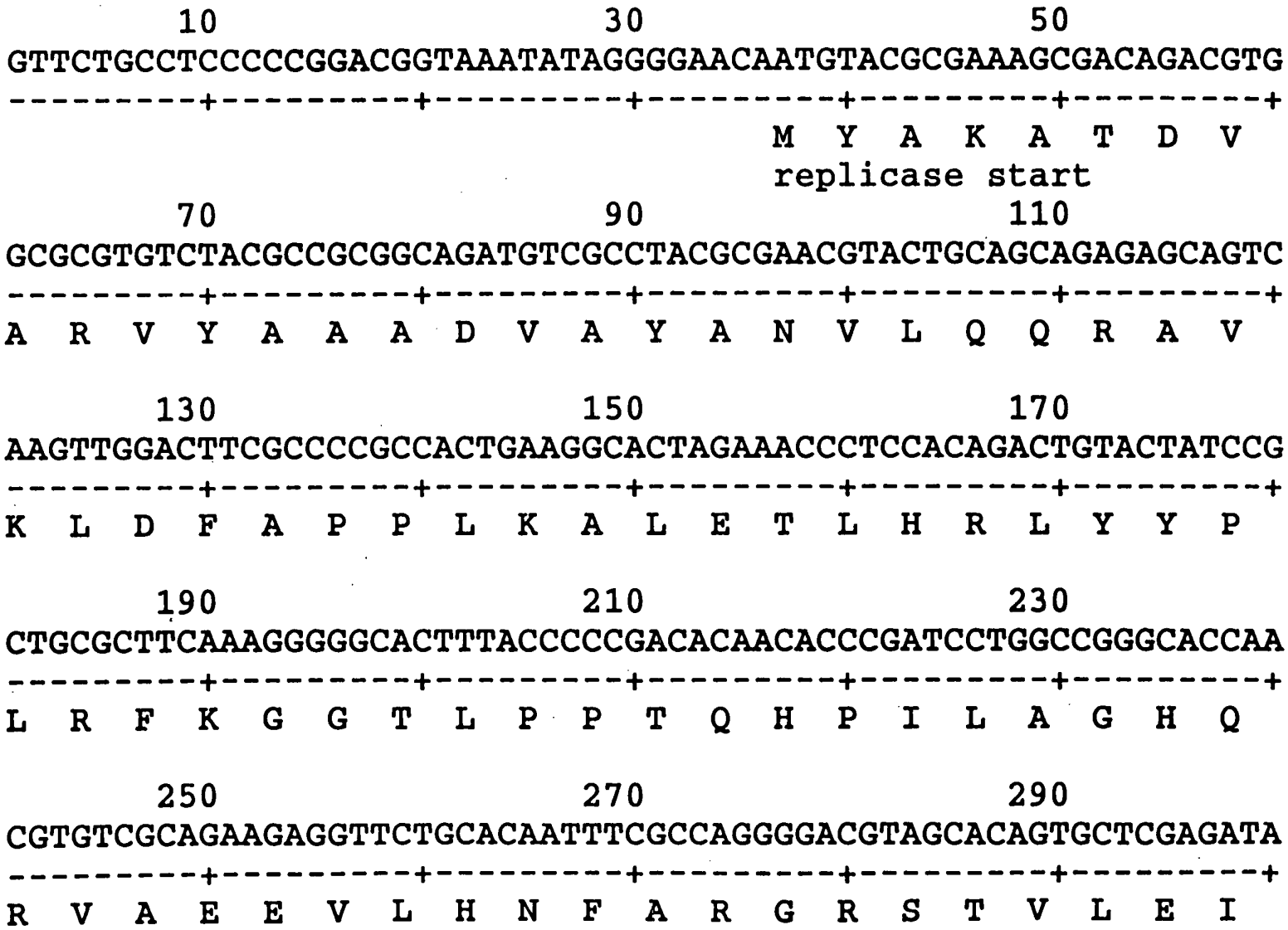

10 30 50
GTTCTGCCTCCCCCGGACGGTAAATATAGGGGAACAATGTACGCGAAAGCGACAGACGTG
M Y A K A T D V
replicase start
70 90 110
GCGCGTGTCTACGCCGCGGCAGATGTCGCCTACGCGAACGTACTGCAGCAGAGAGCAGTC
A R V Y A A A D V A Y A N V L Q Q R A V
130 150 170
AAGTTGGACTTCGCCCCGCCACTGAAGGCACTAGAAACCCTCCACAGACTGTACTATCCG
K L D F A P P L K A L E T L H R L Y Y P
190 210 230
CTGCGCTTCAAAGGGGGCACTTTACCCCCGACACAACACCCGATCCTGGCCGGGCACCAA
L R F K G G T L P P T Q H P I L A G H Q
250 270 290
CGTGTCGCAGAAGAGGTTCTGCACAATTTCGCCAGGGGACGTAGCACAGTGCTCGAGATA
R V A E E V L H N F A R G R S T V L E I

FIG. 2

```
         310                           330                           350
GGGCCGTCTCTGCACAGCGCACTTAAGCTACATGGGGCACCGAACGCCCCCGTCGCAGAC
---------+---------+---------+---------+---------+---------+
G  P  S  L  H  S  A  L  K  L  H  G  A  P  N  A  P  V  A  D

         370                           390                           410
TATCACGGGTGCACCAAGTACGGCACCCGCGACGGCTCGCGACACATTACGGCCTTAGAG
---------+---------+---------+---------+---------+---------+
Y  H  G  C  T  K  Y  G  T  R  D  G  S  R  H  I  T  A  L  E

         430                           450                           470
TCTAGATCCGTCGCCACAGGCCGGCCCGAGTTCAAGGCCGACGCCTCACTGCTCGCCAAC
---------+---------+---------+---------+---------+---------+
S  R  S  V  A  T  G  R  P  E  F  K  A  D  A  S  L  L  A  N

         490                           510                           530
GGCATTGCCTCCCGCACCTTCTGCGTCGACGGAGTCGGCTCTTGCGCGTTCAAATCGCGC
---------+---------+---------+---------+---------+---------+
G  I  A  S  R  T  F  C  V  D  G  V  G  S  C  A  F  K  S  R

         550                           570                           590
GTTGGAATTGCCAATCACTCCCTCTATGACGTGACCCTAGAGGAGCTGGCCAATGCGTTT
---------+---------+---------+---------+---------+---------+
V  G  I  A  N  H  S  L  Y  D  V  T  L  E  E  L  A  N  A  F
```

FIG. 2 Cont'd

```
          610                           630                           650
GAGAACCACGGACTTCACATGGTCCGCGTTCATGCACATGCCAGAAGAGCTGCTCTAC
---------+---------+---------+---------+---------+---------+
E  N  H  G  L  H  M  V  R  A  F  M  H  M  P  E  E  L  L  Y

          670                           690                           710
ATGGACAACGTGGTTAATGCCGAGCTCGGCTACCGCTTCCACGTTATTGAAGAGCCTATG
---------+---------+---------+---------+---------+---------+
M  D  N  V  V  N  A  E  L  G  Y  R  F  H  V  I  E  E  P  M

          730                           750                           770
GCTGTGAAGGACTGCGCATTCCAGGGGGGGGACCTCCGTCTCCACTTCCCTGAGTTGGAC
---------+---------+---------+---------+---------+---------+
A  V  K  D  C  A  F  Q  G  G  D  L  R  L  H  F  P  E  L  D

          790                           810                           830
TTCATCAACGAGAGCCAAGAGCGGCGCATCGAGAGGCTGGCCGCCCGCGGCTCCTACTCC
---------+---------+---------+---------+---------+---------+
F  I  N  E  S  Q  E  R  R  I  E  R  L  A  A  R  G  S  Y  S

          850                           870                           890
AGACGCGCCGTCATTTTCTCCGGCGACGACGACTGGGGTGATGCGTACTTACACGACTTC
---------+---------+---------+---------+---------+---------+
R  R  A  V  I  F  S  G  D  D  D  W  G  D  A  Y  L  H  D  F
```

FIG. 2 Cont'd

```
        910                                930                                950
CACACATGGCTCGCCTACCTACTGGTGAGGAACTACCCCACTCCGTTTGGTTTCTCACTC
---------+---------+---------+---------+---------+---------+
H  T  W  L  A  Y  L  L  V  R  N  Y  P  T  P  F  G  F  S  L

        970                                990                               1010
CATATAGAAGTCCAGAGGCGCCACGGCTCCAGCATTGAGCTGCGCATCACTCGCGCGCCA
---------+---------+---------+---------+---------+---------+
H  I  E  V  Q  R  R  H  G  S  S  I  E  L  R  I  T  R  A  P

       1030                               1050                               1070
CCTGGAGACCGCATGCTGGCCGTCGTCCCAAGGACGTCCCAAGGCCTCTGCAGAATCCCA
---------+---------+---------+---------+---------+---------+
P  G  D  R  M  L  A  V  V  P  R  T  S  Q  G  L  C  R  I  P

       1090                               1110                               1130
AACATCTTTTATTACGCCGACGCGTCGGGCACTGAGCATAAGACCATCCTTACGTCACAG
---------+---------+---------+---------+---------+---------+
N  I  F  Y  Y  A  D  A  S  G  T  E  H  K  T  I  L  T  S  Q

       1150                               1170                               1190
CACAAAGTCAACATGCTGCTCAATTTTATGCAAACGCGTCCTGAGAAGGAACTAGTCGAC
---------+---------+---------+---------+---------+---------+
H  K  V  N  M  L  L  N  F  M  Q  T  R  P  E  K  E  L  V  D
```

FIG. 2 Cont'd

```
        1210                1230                1250
ATGACCGTCTTGATGTCGTTCGCGCGCTAGGCTGCGCGATCGTGGTCGCCTCAGAA
---------+---------+---------+---------+---------+---------+
M  T  V  L  M  S  F  A  R  A  R  L  R  A  I  V  V  A  S  E

        1270                1290                1310
GTCACCGAGAGCTCCTGGAACATCTCACCGGCTGACCTGGTCCGCACTGTCGTGTCTCTT
---------+---------+---------+---------+---------+---------+
V  T  E  S  S  W  N  I  S  P  A  D  L  V  R  T  V  V  S  L

        1330                1350                1370
TACGTCCTCCACATCATCGAGCGCCGAAGGGCTGCGGTCGCTGTCAAGACCGCCAAGGAC
---------+---------+---------+---------+---------+---------+
Y  V  L  H  I  I  E  R  R  R  A  A  V  A  V  K  T  A  K  D

        1390                1410                1430
GACGTCTTTGGAGAGACTTCGTTCTGGGAGAGTCTCAAGCACGTCTTGGGCTCCTGTTGC
---------+---------+---------+---------+---------+---------+
D  V  F  G  E  T  S  F  W  E  S  L  K  H  V  L  G  S  C  C

        1450                1470                1490
GGTCTGCGCAACCTCAAAGGCACCGACGTCGTCTTTACTAAGCGCGTCGTCGATAAGTAC
---------+---------+---------+---------+---------+---------+
G  L  R  N  L  K  G  T  D  V  V  F  T  K  R  V  V  D  K  Y
```

FIG. 2 Cont'd

```
      1510                  1530                  1550
CGAGTCCACTCGCTCGGAGACATAATCTGCGACGTCCGCCTGTCCCCTGAACAGGTCGGC
---------+---------+---------+---------+---------+---------+
R  V  H  S  L  G  D  I  I  C  D  V  R  L  S  P  E  Q  V  G

      1570                  1590                  1610
TTCCTGCCGTCCCGCGTACCACCTGCCCGCGTCTTTCACGACAGGGAAGAGCTTGAGGTC
---------+---------+---------+---------+---------+---------+
F  L  P  S  R  V  P  P  A  R  V  F  H  D  R  E  E  L  E  V

      1630                  1650                  1670
CTTCGCGAAGCTGGCTGCTACAACGAACGTCCGGTACCTTCCACTCCTCCTGTGGAGGAG
---------+---------+---------+---------+---------+---------+
L  R  E  A  G  C  Y  N  E  R  P  V  P  S  T  P  P  V  E  E

      1690                  1710                  1730
CCCCAAGGTTTCGACGCCGACTTGTGGCACGCGACCGCGGCCTCACTCCCCGAGTACCGC
---------+---------+---------+---------+---------+---------+
P  Q  G  F  D  A  D  L  W  H  A  T  A  A  S  L  P  E  Y  R

      1750                  1770                  1790
GCCACCTTGCAGGCAGGTCTCAACACCGACGTCAAGCAGCTCAAGATCACCCTCGAGAAC
---------+---------+---------+---------+---------+---------+
A  T  L  Q  A  G  L  N  T  D  V  K  Q  L  K  I  T  L  E  N
```

FIG. 2 Cont'd

```
       1810                1830                1850
GCCCTCAAGACCATCGACGGGCTCACCCTCTCCCCAGTCAGAGGCCTCGAGATGTACGAG
---------+---------+---------+---------+---------+---------+
A  L  K  T  I  D  G  L  T  L  S  P  V  R  G  L  E  M  Y  E

       1870                1890                1910
GGCCCGCCAGGCAGCGGCAAGACGGGCACCCTCATCGCCGCCCTTGAGGCCGCGGGCGGT
---------+---------+---------+---------+---------+---------+
G  P  P  G  S  G  K  T  G  T  L  I  A  A  L  E  A  A  G  G

       1930                1950                1970
AAAGCACTTTACGTGGCACCCACCAGAGAACTGAGAGAGGCTATGGACCGGCGGATCAAA
---------+---------+---------+---------+---------+---------+
K  A  L  Y  V  A  P  T  R  E  L  R  E  A  M  D  R  R  I  K

       1990                2010                2030
CCGCCGTCCGCCTCGGCTACGCAACATGTCGCCCTTGCGATTCTCCGTCGTGCCACCGCC
---------+---------+---------+---------+---------+---------+
P  P  S  A  S  A  T  Q  H  V  A  L  A  I  L  R  R  A  T  A

       2050                2070                2090
GAGGGCGCCCCTTTCGCTACCGTGGTTATCGACGAGTGCTTCATGTTCCCGCTCGTGTAC
---------+---------+---------+---------+---------+---------+
E  G  A  P  F  A  T  V  V  I  D  E  C  F  M  F  P  L  V  Y
```

FIG. 2 Cont'd

```
        2110                2130                2150
GTCGCGATCGTGCACGCCTTGTCCCCGAGCTCACGAATAGTCCTTGTAGGGGACGTCCAC
---------+---------+---------+---------+---------+---------+
V  A  I  V  H  A  L  S  P  S  S  R  I  V  L  V  G  D  V  H

        2170                2190                2210
CAAATCGGGTTTATAGACTTCCAAGGCACAAGCGCGAACATGCCGCTCGTTCGCGACGTC
---------+---------+---------+---------+---------+---------+
Q  I  G  F  I  D  F  Q  G  T  S  A  N  M  P  L  V  R  D  V

        2230                2250                2270
GTTAAGCAGTGCCGTCGGCGCACTTTCAACCAAACCAAGCGCTGTCCGGCCGACGTCGTT
---------+---------+---------+---------+---------+---------+
V  K  Q  C  R  R  R  T  F  N  Q  T  K  R  C  P  A  D  V  V

        2290                2310                2330
GCCACCACGTTTTTCCAGAGCTTGTACCCCGGGTGCACAACCACCTCAGGGTGCGTCGCA
---------+---------+---------+---------+---------+---------+
A  T  T  F  F  Q  S  L  Y  P  G  C  T  T  T  S  G  C  V  A

        2350                2370                2390
TCCATCAGCCACGTCGCCCCAGACTACCGCAACAGCCAGGCGCAAACGCTCTGCTTCACG
---------+---------+---------+---------+---------+---------+
S  I  S  H  V  A  P  D  Y  R  N  S  Q  A  Q  T  L  C  F  T
```

FIG. 2 Cont'd

```
        2410                      2430                      2450
CAGGAGGAAAAGTCGCGCCACGGGGCTGAGGGCGCGATGACTGTGCACGAAGCGCAGGGA
---------+---------+---------+---------+---------+---------+
Q  E  E  K  S  R  H  G  A  E  G  A  M  T  V  H  E  A  Q  G

        2470                      2490                      2510
CGCACTTTTGCGTCTGTCATTCTGCATTACAACGGCTCCACAGCAGAGCAGAAGCTCCTC
---------+---------+---------+---------+---------+---------+
R  T  F  A  S  V  I  L  H  Y  N  G  S  T  A  E  Q  K  L  L

        2530                      2550                      2570
GCTGAGAAGTCGCACCTTCTAGTCGGCATCACGCGCCACACCAACCACCTGTACATCCGC
---------+---------+---------+---------+---------+---------+
A  E  K  S  H  L  L  V  G  I  T  R  H  T  N  H  L  Y  I  R

        2590                      2610                      2630
GACCCGACAGGTGACATTGAGAGACAACTCAACCATAGCGCGAAAGCCGAGGTGTTTACA
---------+---------+---------+---------+---------+---------+
D  P  T  G  D  I  E  R  Q  L  N  H  S  A  K  A  E  V  F  T

        2650                      2670                      2690
GACATCCCTGCACCCCTGGAGATCACGACTGTCAAACCGAGTGAAGAGGTGCAGCGCAAC
---------+---------+---------+---------+---------+---------+
D  I  P  A  P  L  E  I  T  T  V  K  P  S  E  E  V  Q  R  N
```

FIG. 2 Cont'd

```
      2710                  2730                  2750
GAAGTGATGGCAACGATACCCCCGCAGAGTGCCACGCCGCACGGAGCAATCCATCTGCTC
---------+---------+---------+---------+---------+---------+
E  V  M  A  T  I  P  P  Q  S  A  T  P  H  G  A  I  H  L  L

      2770                  2790                  2810
CGCAAGAACTTCGGGGACCAACCCGACTGTGGCTGTGTCGCTTTGGCGAAGACCGGCTAC
---------+---------+---------+---------+---------+---------+
R  K  N  F  G  D  Q  P  D  C  G  C  V  A  L  A  K  T  G  Y

      2830                  2850                  2870
GAGGTGTTTGGCGGTCGTGCCAAAATCAACGTAGAGCTTGCCGAACCCGACGCGACCCCG
---------+---------+---------+---------+---------+---------+
E  V  F  G  G  R  A  K  I  N  V  E  L  A  E  P  D  A  T  P

      2890                  2910                  2930
AAGCCGCATAGGGCGTTCCAGGAAGGGGTACAGTGGGTCAAGGTCACCAACGCGTCTAAC
---------+---------+---------+---------+---------+---------+
K  P  H  R  A  F  Q  E  G  V  Q  W  V  K  V  T  N  A  S  N

      2950                  2970                  2990
AAACACCAGGCGCTCCAGACGCTGTTGTCCCGCTACACCAAGCGAAGCGCTGACCTGCCG
---------+---------+---------+---------+---------+---------+
K  H  Q  A  L  Q  T  L  L  S  R  Y  T  K  R  S  A  D  L  P
```

FIG. 2 Cont'd

```
      3010                 3030                 3050
CTACACGAAGCTAAGGAGGACGTCAAACGCATGCTAAACTCGCTTGACCGACATTGGGAC
---------+---------+---------+---------+---------+---------+
L  H  E  A  K  E  D  V  K  R  M  L  N  S  L  D  R  H  W  D

      3070                 3090                 3110
TGGACTGTCACTGAAGACGCCCGTGACCGAGCTGTCTTCGAGACCCAGCTCAAGTTCACC
---------+---------+---------+---------+---------+---------+
W  T  V  T  E  D  A  R  D  R  A  V  F  E  T  Q  L  K  F  T

      3130                 3150                 3170
CAACGCGGCGGCACCGTCGAAGACCTGCTGGAGCCAGACGACCCCTACATCCGTGACATA
---------+---------+---------+---------+---------+---------+
Q  R  G  G  T  V  E  D  L  L  E  P  D  D  P  Y  I  R  D  I

      3190                 3210                 3230
GACTTCCTTATGAAGACTCAGCAGAAAGTGTCGCCCAAGCCGATCAATACGGGCAAGGTC
---------+---------+---------+---------+---------+---------+
D  F  L  M  K  T  Q  Q  K  V  S  P  K  P  I  N  T  G  K  V

      3250                 3270                 3290
GGGCAGGGGATCGCCGCTCACTCAAAGTCTCTCAACTTCGTCCTCGCCGCTTGGATACGC
---------+---------+---------+---------+---------+---------+
G  Q  G  I  A  A  H  S  K  S  L  N  F  V  L  A  A  W  I  R
```

FIG. 2 Cont'd

```
        3310                3330                3350
ATACTCGAGGAGATACTCCGTACCGGGAGCCGCACGGTCCGGTACAGCAACGGTCTCCCC
---------+---------+---------+---------+---------+---------+
I  L  E  E  I  L  R  T  G  S  R  T  V  R  Y  S  N  G  L  P

        3370                3390                3410
GACGAAGAAGAGGCCATGCTGCTCGAAGCGAAGATCAATCAAGTCCCACACGCCACGTTC
---------+---------+---------+---------+---------+---------+
D  E  E  E  A  M  L  L  E  A  K  I  N  Q  V  P  H  A  T  F

        3430                3450                3470
GTCTCGGCGGACTGGACCGAGTTTGACACCGCCCACAATAACACGAGTGAGCTGCTCTTC
---------+---------+---------+---------+---------+---------+
V  S  A  D  W  T  E  F  D  T  A  H  N  N  T  S  E  L  L  F

        3490                3510                3530
GCCGCCCTTTTAGAGCGCATCGGCACGCCTGCAGCTGCCGTTAATCTATTCAGAGAACGG
---------+---------+---------+---------+---------+---------+
A  A  L  L  E  R  I  G  T  P  A  A  A  V  N  L  F  R  E  R

        3550                3570                3590
TGTGGGAAACGCACCTTGCGAGCGAAGGGTCTAGGCTCCGTTGAAGTCGACGGTCTGCTC
---------+---------+---------+---------+---------+---------+
C  G  K  R  T  L  R  A  K  G  L  G  S  V  E  V  D  G  L  L
```

FIG. 2 Cont'd

```
      3610                  3630                  3650
GACTCCGGCGCAGCTTGGACGCCTTGCCGCAACACCATCTTCTCTGCCGCCGTCATGCTC
--------+---------+---------+---------+---------+---------+
D  S  G  A  A  W  T  P  C  R  N  T  I  F  S  A  A  V  M  L

      3670                  3690                  3710
ACGCTCTTCCGCGGCGTCAAGTTCGCAGCTTTCAAAGGCGACGACTCGCTCCTCTGTGGT
--------+---------+---------+---------+---------+---------+
T  L  F  R  G  V  K  F  A  A  F  K  G  D  D  S  L  L  C  G

      3730                  3750                  3770
AGCCATTACCTCCGTTTCGACGCTAGCCGCCTTCACATGGGCGAACGTTACAAGACCAAA
--------+---------+---------+---------+---------+---------+
S  H  Y  L  R  F  D  A  S  R  L  H  M  G  E  R  Y  K  T  K

      3790                  3810                  3830
CATTTGAAGGTCGAGGTGCAGAAAATCGTGCCGTACATCGGACTCCTCGTCTCCGCTGAG
--------+---------+---------+---------+---------+---------+
H  L  K  V  E  V  Q  K  I  V  P  Y  I  G  L  L  V  S  A  E

      3850                  3870                  3890
CAGGTCGTCCTCGACCCTGTCAGGAGCGCTCTCAAGATATTTGGGCGCTGCTACACAAGC
--------+---------+---------+---------+---------+---------+
Q  V  V  L  D  P  V  R  S  A  L  K  I  F  G  R  C  Y  T  S
```

FIG. 2 Cont'd

```
          3910                3930                3950
GAACTCCTTTACTCCAAGTACGTGGAGGCTGTGAGAGACATCACCAAGGGCTGGAGTGAC
---------+---------+---------+---------+---------+---------+
E  L  L  Y  S  K  Y  V  E  A  V  R  D  I  T  K  G  W  S  D

          3970                3990                4010
GCCCGCTACCACAGCCTCCTGTGCCACATGTCAGCATGCTACTACAATTACGCGCCGGAG
---------+---------+---------+---------+---------+---------+
A  R  Y  H  S  L  L  C  H  M  S  A  C  Y  Y  N  Y  A  P  E

          4030                4050                4070
TCTGCGGCGTACATCATCGACGCTGTTGTTCGCTTTGGGCGCGGCGACTTCCCGTTTGAA
---------+---------+---------+---------+---------+---------+
S  A  A  Y  I  I  D  A  V  V  R  F  G  R  G  D  F  P  F  E

          4090                4110                4130
CAACTGCGCGTGGTGCGTGCCCATGTGCAGGCACCCGACGCTTACAGCAGCACGTATCCG
---------+---------+---------+---------+---------+---------+
Q  L  R  V  V  R  A  H  V  Q  A  P  D  A  Y  S  S  T  Y  P

          4150                4170                4190
GCTAACGTGCGCGCATCGTGCCTTGACCACGTCTTCGAGCCCCGCCAGGCCGCCGCCCCG
---------+---------+---------+---------+---------+---------+
A  N  V  R  A  S  C  L  D  H  V  F  E  P  R  Q  A  A  A  P
```

FIG. 2 Cont'd

```
      4210                  4230                  4250
GCAGGTTTCGTTGCGACATGTGCGAAGCCGGAAACGCCTTCTTCACTTACCGCGAAAGCT
---------+---------+---------+---------+---------+---------+
A  G  F  V  A  T  C  A  K  P  E  T  P  S  S  L  T  A  K  A
                  M  C  E  A  G  N  A  F  F  T  Y  R  E  S  W
                  P11a start
      4270                  4290                  4310
GGTGTTTCTGCGACTACAAGCCACGTTGCGACTGGGACTGCGCCCCCGGAGTCTCCATGG
---------+---------+---------+---------+---------+---------+
G  V  S  A  T  T  S  H  V  A  T  G  T  A  P  P  E  S  P  W
   C  F  C  D  Y  K  P  R  C  D  W  D  C  A  P  G  V  S  M  G

      4330                  4350                  4370
GATGCACCTGCAGCCAACAGCTTTTCGGAGTTATTGACACCGGAGACCCCGTCCACATCA
---------+---------+---------+---------+---------+---------+
D  A  P  A  A  N  S  F  S  E  L  L  T  P  E  T  P  S  T  S
   C  T  C  S  Q  Q  L  F  G  V  I  D  T  G  D  P  V  H  I  I

      4390                  4410                  4430
TCCTCGCCGTCATCGTCTTCATCGGACTCCTCTACATCGTGTGGAAGGTCGCTCAGTGGT
---------+---------+---------+---------+---------+---------+
S  S  P  S  S  S  S  S  D  S  S  T  S  C  G  R  S  L  S  G
   L  A  V  I  V  F  I  G  L  L  Y  I  V  W  K  V  A  Q  W  W
```

FIG. 2 Cont'd

```
      4450                4470                4490
GGAGACACCGCAAGGACCACAGAAGACTTGAACAGCAGAAAGCCGCCTTCGCAAGACAGG
---------+---------+---------+---------+---------+---------+
G  D  T  A  R  T  T  E  D  L  N  S  R  K  P  P  S  Q  D  R
 R  H  R  K  D  H  R  R  L  E  Q  Q  K  A  A  F  A  R  Q  A

      4510                4530                4550
CAATCACGCTCGTCTGAATGTCTGGACAGAAGCGGAGAAAGGACAGGCAGTTCGTTAACT
---------+---------+---------+---------+---------+---------+
Q  S  R  S  S  E  C  L  D  R  S  G  E  R  T  G  S  S  L  T
 I  T  L  V  *  M  S  G  Q  K  R  R  K  D  R  Q  F  V  N  C
                P11b start
      4570                4590                4610
GCCCCCACTGCTCCGAGCCCCTCATTCTCATTTTCGGAAAGAGCTCGACTGGCGACCGGG
---------+---------+---------+---------+---------+---------+
A  P  T  A  P  S  P  S  F  S  F  S  E  R  A  R  L  A  T  G
 P  H  C  S  E  P  L  I  L  I  F  G  K  S  S  T  G  D  R  A

      4630                4650                4670
CCGACTGTCGCCGCTGCGACATCACCTTCGGCAACCCCATCCTGCGCCACGGACCAGGTT
---------+---------+---------+---------+---------+---------+
P  T  V  A  A  A  T  S  P  S  A  T  P  S  C  A  T  D  Q  V
 D  C  R  R  C  D  I  T  F  G  N  P  I  L  R  H  G  P  G  C
```

FIG. 2 Cont'd

```
       4690                4710                4730
GCCGCGAGGACCACGCCGGACTTTGCGCCTTTCCTGGGTTCCCAGTCTGCCCGTGCTGTC
---------+---------+---------+---------+---------+---------+
A  A  R  T  T  P  D  F  A  P  F  L  G  S  Q  S  A  R  A  V
  R  E  D  H  A  G  L  C  A  F  P  G  F  P  V  C  P  C  C  L

       4750                4770                4790
TCGAAGCCGTACCGGCCCCCCACGACTGCCCGTTGGAAAGAAGTCACCCCGCTCCACGCG
---------+---------+---------+---------+---------+---------+
S  K  P  Y  R  P  P  T  T  A  R  W  K  E  V  T  P  L  H  A
  E  A  V  P  A  P  H  D  C  P  L  E  R  S  H  P  A  P  R  V

       4810                4830                4850
TGGAAGGGCGTGACCGGAGACCGACCGGAAGTCAGGGAGGACCCGGAGACAGCGGCGGTC
---------+---------+---------+---------+---------+---------+
W  K  G  V  T  G  D  R  P  E  V  R  E  D  P  E  T  A  A  V
  E  G  R  D  R  R  P  T  G  S  Q  G  G  P  G  D  S  G  G  R

       4870                4890                4910
GTCCAGGCTCTGATCAGCGGCCGTTATCCTCAGAAGACGAAGCTTTCCTCCGACGCATCC
---------+---------+---------+---------+---------+---------+
V  Q  A  L  I  S  G  R  Y  P  Q  K  T  K  L  S  S  D  A  S
  P  G  S  D  Q  R  P  L  S  S  E  D  E  A  F  L  R  R  I  Q
```

FIG. 2 Cont'd

```
      4930                    4950                    4970
AAAGGCTACTCAAGAACTAAGGGATGCTCACAATCCACCTCTTTTCCTGCCCCGAGTGCG
--------+---------+---------+---------+---------+---------+
K  G  Y  S  R  T  K  G  C  S  Q  S  T  S  F  P  A  P  S  A
   R  L  L  K  N  *     M  L  T  I  H  L  F  S  C  P  E  C  G
                        P14 start
      4990                    5010                    5030
GATTACCAGGCCCGCGACTGCCAGACAGTCCGAGTCTGCCGCGCCGCTGCAGAGATGGCG
--------+---------+---------+---------+---------+---------+
D  Y  Q  A  R  D  C  Q  T  V  R  V  C  R  A  A  A  E  M  A
   L  P  G  P  R  L  P  D  S  P  S  L  P  R  R  C  R  D  G  A

      5050                    5070                    5090
CGCTCATGTATTCACGAGCCGTTGGCTTCATCTGCCGCCAGTGCCGACTTGAAGCGCATA
--------+---------+---------+---------+---------+---------+
R  S  C  I  H  E  P  L  A  S  S  A  A  S  A  D  L  K  R  I
   L  M  Y  S  R  A  V  G  F  I  C  R  Q  C  R  L  E  A  H  T

      5110                    5130                    5150
CGCTCTACCTCGGACTCTGTTCCCGATGTAAAGATCAGCAAGAGCGCATGAAGGAACAAA
--------+---------+---------+---------+---------+---------+
R  S  T  S  D  S  V  P  D  V  K  I  S  K  S  A  *
   L  Y  L  G  L  C  S  R  C  K  D  Q  Q  E  R  M  K  E  Q  N
```

FIG. 2 Cont'd

```
      5170                    5190                    5210
ATTAGTTTCCTTGTTCGTAAACAAGGTGGTCCCTCCCATTGAGGTAAAGACTCTGGTGAG
---------+---------+---------+---------+---------+---------+
   *

      5230                    5250                    5270
TCCTCAACGTTACTCGTTGAGTCTGCTGCGGTTCGATTCCATTCCCAAGCAGCAAAGGGT
---------+---------+---------+---------+---------+---------+

      5290                    5310
GCGCAACTAGTACGGCGCCCCCTGGGATACCA
---------+---------+---------+--
```

FIG. 2 Cont'd

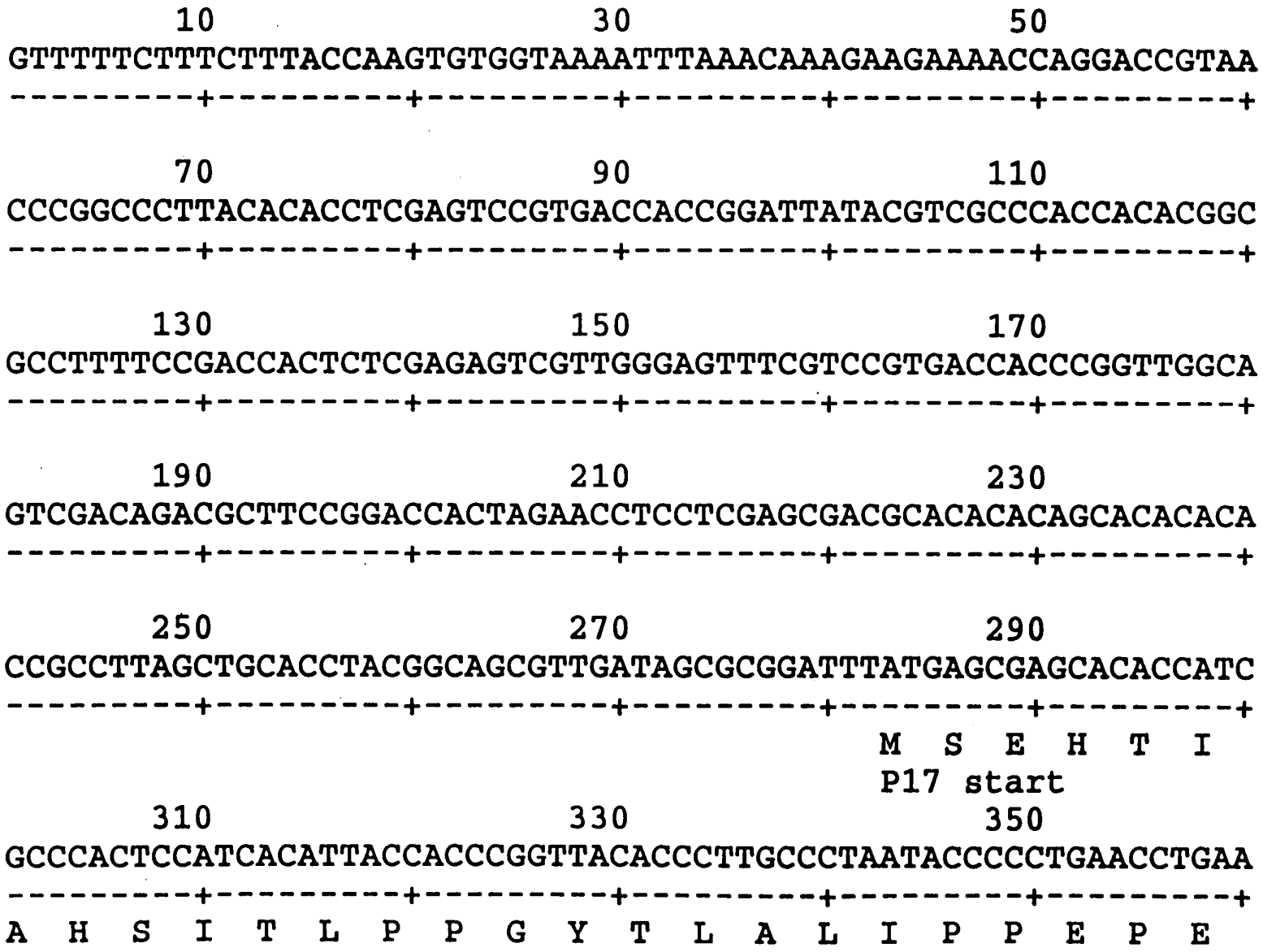

10
30
50
GTTTTTCTTTCTTTACCAAGTGTGGTAAAATTTAAACAAAGAAGAAAACCAGGACCGTAA
70
90
110
CCCGGCCCTTACACACCTCGAGTCCGTGACCACCGGATTATACGTCGCCCACCACACGGC
130
150
170
GCCTTTTCCGACCACTCTCGAGAGTCGTTGGGAGTTTCGTCCGTGACCACCCGGTTGGCA
190
210
230
GTCGACAGACGCTTCCGGACCACTAGAACCTCCTCGAGCGACGCACACACAGCACACACA
250
270
290
CCGCCTTAGCTGCACCTACGGCAGCGTTGATAGCGCGGATTTATGAGCGAGCACACCATC
M S E H T I
P17 start
310
330
350
GCCCACTCCATCACATTACCACCCGGTTACACCCTTGCCCTAATACCCCCTGAACCTGAA
A H S I T L P P G Y T L A L I P P E P E

FIG. 3a

```
      370                 390                 410
GCAGGATGGGAGATGCTGGAGTGGCGTCACAGCGACCTCACAACCGTCGCGGAACCCGTA
---------+---------+---------+---------+---------+---------+
A  G  W  E  M  L  E  W  R  H  S  D  L  T  T  V  A  E  P  V
     M  G  D  A  G  V  A  S  Q  R  P  H  N  R  R  G  T  R  N
     P71 start
      430                 450                 470
ACGTTCGGGTCAGCGCCAACACCGTCACCGTCAATGGTAGAAGAAACCAACGGCGTCGGA
---------+---------+---------+---------+---------+---------+
T  F  G  S  A  P  T  P  S  P  S  M  V  E  E  T  N  G  V  G
  V  R  V  S  A  N  T  V  T  V  N  G  R  R  N  Q  R  R  R  T

      490                 510                 530
CCGGAAGGCAAGTTTCTCCCCCTGACAATTTCACCGCTGCTGCACAAGACCTCGCGCAAA
---------+---------+---------+---------+---------+---------+
P  E  G  K  F  L  P  L  T  I  S  P  L  L  H  K  T  S  R  K
  G  R  Q  V  S  P  P  D  N  F  T  A  A  A  Q  D  L  A  Q  S

      550                 570                 590
GCCTTGACGCCAACACCGTCACTTTCCCCGCTAACATCTCTAGCATGCCCGAATTCCGGA
---------+---------+---------+---------+---------+---------+
A  L  T  P  T  P  S  L  S  P  L  T  S  L  A  C  P  N  S  G
  L  D  A  N  T  V  T  F  P  A  N  I  S  S  M  P  E  F  R  N
```

FIG. 3a Cont'd

```
          610                 630                 650
ATTGGGCCAAGGGAAAGATCGACCTCGACTCCGATTCCATCGGCTGGTACTTCAAGTACC
---------+---------+---------+---------+---------+---------+
I  G  P  R  E  R  S  T  S  T  P  I  P  S  A  G  T  S  S  T
  W  A  K  G  K  I  D  L  D  S  D  S  I  G  W  Y  F  K  Y  L

          670                 690                 710
TTGACCCAGCGGGTGCTACAGAGTCTGCGCGCCGTCGGCGAGTACTCGAAGATCCCTG
---------+---------+---------+---------+---------+---------+
L  T  Q  R  V  L  Q  S  L  R  A  P  S  A  S  T  R  R  S  L
  D  P  A  G  A  T  E  S  A  R  A  V  G  E  Y  S  K  I  P  D

          730                 750                 770
ACGGCCTCGTCAAGTTCTCCGTCGACGCAGAGATAAGAGAGATCTATAACGAGGAGTGCC
---------+---------+---------+---------+---------+---------+
T  A  S  S  S  S  P  S  T  Q  R  *
  G  L  V  K  F  S  V  D  A  E  I  R  E  I  Y  N  E  E  C  P

          790                 810                 830
CCGTCGTCACTGACGTGTCCGTCCCCCTCGACGGCCGCCAGTGGAGCCTCTCGATTTTCT
---------+---------+---------+---------+---------+---------+
  V  V  T  D  V  S  V  P  L  D  G  R  Q  W  S  L  S  I  F  S
```

FIG. 3a Cont'd

```
          850                 870                 890
CCTTTCCGATGTTCAGAACCGCCTACGTCGCCGTAGCGAACGTCGAGAACAAGGAGATGT
---------+---------+---------+---------+---------+---------+
 F  P  M  F  R  T  A  Y  V  A  V  A  N  V  E  N  K  E  M  S

          910                 930                 950
CGCTCGACGTTGTCAACGACCTCATCGAGTGGCTCAACAATCTCGCCGACTGGCGTTATG
---------+---------+---------+---------+---------+---------+
 L  D  V  V  N  D  L  I  E  W  L  N  N  L  A  D  W  R  Y  V

          970                 990                1010
TCGTTGACTCTGAACAGTGGATTAACTTCACCAATGACACCACGTACTACGTCCGCATCC
---------+---------+---------+---------+---------+---------+
 V  D  S  E  Q  W  I  N  F  T  N  D  T  T  Y  Y  V  R  I  R

         1030                1050                1070
GCGTTCTACGTCCAACCTACGACGTTCCAGACCCCACAGAGGGCCTTGTTCGCACAGTCT
---------+---------+---------+---------+---------+---------+
 V  L  R  P  T  Y  D  V  P  D  P  T  E  G  L  V  R  T  V  S

         1090                1110                1130
CAGACTACCGCCTCACTTATAAGGCGATAACATGTGAAGCCAACATGCCAACACTCGTCG
---------+---------+---------+---------+---------+---------+
 D  Y  R  L  T  Y  K  A  I  T  C  E  A  N  M  P  T  L  V  D
```

FIG. 3a Cont'd

```
         1150                1170                1190
ACCAAGGCTTTTGGATCGGCGGCCAGTACGCTCTCACCCCGACTAGCCTACCGCAGTACG
---------+---------+---------+---------+---------+---------+
 Q  G  F  W  I  G  G  Q  Y  A  L  T  P  T  S  L  P  Q  Y  D

         1210                1230                1250
ACGTCAGCGAGGCCTACGCTCTGCACACTTTGACCTTCGCCAGACCATCCAGCGCCGCTG
---------+---------+---------+---------+---------+---------+
 V  S  E  A  Y  A  L  H  T  L  T  F  A  R  P  S  S  A  A  A

         1270                1290                1310
CACTCGCGTTTGTGTGGGCAGGTTTGCCACAGGGTGGCACTGCGCCTGCAGGCACTCCAG
---------+---------+---------+---------+---------+---------+
 L  A  F  V  W  A  G  L  P  Q  G  G  T  A  P  A  G  T  P  A

         1330                1350                1370
CCTGGGAGCAGGCATCCTCGGGTGGCTACCTCACCTGGCGCCACAACGGTACTACTTTCC
---------+---------+---------+---------+---------+---------+
 W  E  Q  A  S  S  G  G  Y  L  T  W  R  H  N  G  T  T  F  P

         1390                1410                1430
CAGCTGGCTCCGTTAGCTACGTTCTCCCTGAGGGTTTCGCCCTTGAGCGCTACGACCCGA
---------+---------+---------+---------+---------+---------+
 A  G  S  V  S  Y  V  L  P  E  G  F  A  L  E  R  Y  D  P  N
```

FIG. 3a Cont'd

```
     1450                1470                1490
ACGACGGCTCTTGGACCGACTTCGCTTCCGCAGGAGACACCGTCACTTTCCGGCAGGTCG
---------+---------+---------+---------+---------+---------+
  D  G  S  W  T  D  F  A  S  A  G  D  T  V  T  F  R  Q  V  A

     1510                1530                1550
CCGTCGACGAGGTCGTTGTGACCAACAACCCCGCCGGCGGCGGCAGCGCCCCCACCTTCA
---------+---------+---------+---------+---------+---------+
  V  D  E  V  V  V  T  N  N  P  A  G  G  G  S  A  P  T  F  T

     1570                1590                1610
CCGTGAGAGTGCCCCCTTCAAACGCTTACACCAACACCGTGTTTAGGAACACGCTCTTAG
---------+---------+---------+---------+---------+---------+
  V  R  V  P  P  S  N  A  Y  T  N  T  V  F  R  N  T  L  L  E

     1630                1650                1670
AGACTCGACCCTCCTCTCGTAGGCTCGAACTCCCTATGCCACCTGCTGACTTTGGACAGA
---------+---------+---------+---------+---------+---------+
  T  R  P  S  S  R  R  L  E  L  P  M  P  P  A  D  F  G  Q  T

     1690                1710                1730
CGGTCGCCAACAACCCGAAGATCGAGCAGTCGCTTCTTAAAGAAACACTTGGCTGCTATT
---------+---------+---------+---------+---------+---------+
  V  A  N  N  P  K  I  E  Q  S  L  L  K  E  T  L  G  C  Y  L
```

FIG. 3a Cont'd

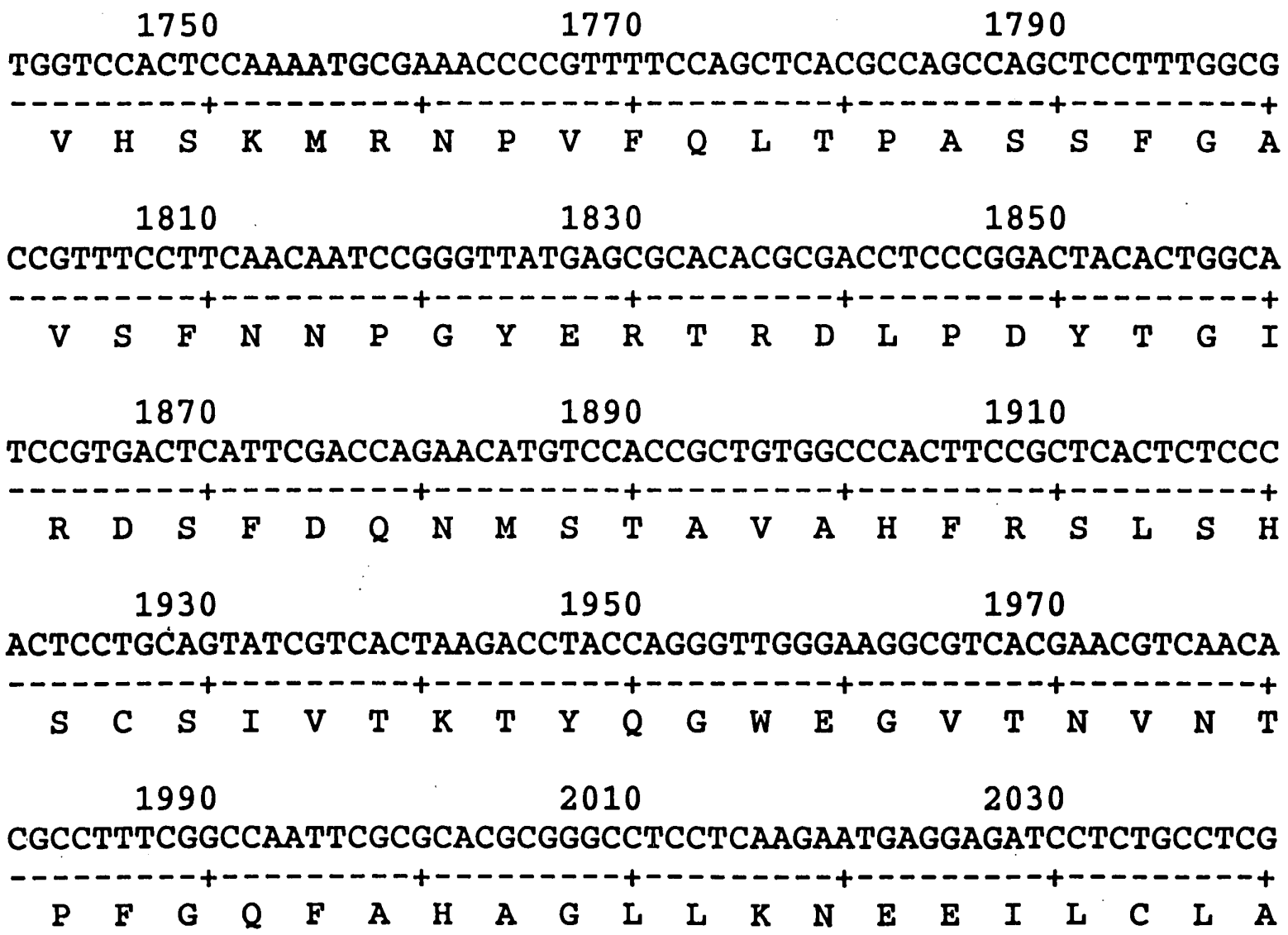

1750 1770 1790
TGGTCCACTCCAAAATGCGAAACCCCGTTTTCCAGCTCACGCCAGCCAGCTCCTTTGGCG
V H S K M R N P V F Q L T P A S S F G A
1810 1830 1850
CCGTTTCCTTCAACAATCCGGGTTATGAGCGCACACGCGACCTCCCGGACTACACTGGCA
V S F N N P G Y E R T R D L P D Y T G I
1870 1890 1910
TCCGTGACTCATTCGACCAGAACATGTCCACCGCTGTGGCCCACTTCCGCTCACTCTCCC
R D S F D Q N M S T A V A H F R S L S H
1930 1950 1970
ACTCCTGCAGTATCGTCACTAAGACCTACCAGGGTTGGGAAGGCGTCACGAACGTCAACA
S C S I V T K T Y Q G W E G V T N V N T
1990 2010 2030
CGCCTTTCGGCCAATTCGCGCACGCGGGCCTCCTCAAGAATGAGGAGATCCTCTGCCTCG
P F G Q F A H A G L L K N E E I L C L A

FIG. 3a Cont'd

```
        2050                                    2070                                    2090
CCGACGACCTGGCCACCCGTCTCACAGGTGTCTACCCCGCCACTGACAACTTCGCGGCCG
---------+---------+---------+---------+---------+---------+
 D  D  L  A  T  R  L  T  G  V  Y  P  A  T  D  N  F  A  A  A

        2110                                    2130                                    2150
CCGTTTCTGCCTTCGCCGCGAACATGCTGTCCTCCGTGCTGAAGTCGGAGGCAACGTCCT
---------+---------+---------+---------+---------+---------+
 V  S  A  F  A  A  N  M  L  S  S  V  L  K  S  E  A  T  S  S

        2170                                    2190                                    2210
CCATCATCAAGTCCGTTGGCGAGACTGCCGTCGGCGCGGCTCAGTCCGGCCTCGCGAAGC
---------+---------+---------+---------+---------+---------+
 I  I  K  S  V  G  E  T  A  V  G  A  A  Q  S  G  L  A  K  L

        2230                                    2250                                    2270
TACCCGGACTGCTAATGAGTGTACCAGGGAAGATTGCCGCGCGTGTCCGCGCGCGCCGAG
---------+---------+---------+---------+---------+---------+
 P  G  L  L  M  S  V  P  G  K  I  A  A  R  V  R  A  R  R  A

        2290                                    2310                                    2330
CGCGCCGCCGCGCCGCTCGTGCCAATTAGTTTGCTCGCTCCTGTTTCGCCGTTTCGTAAA
---------+---------+---------+---------+---------+---------+
 R  R  R  A  A  R  A  N  *
```

FIG. 3a Cont'd

```
      2350                  2370                  2390
ACGGCGTGGTCCCGCACATTACGCGTACCCTAAAGACTCTGGTGAGTCCCCGTCGTTACA
---------+---------+---------+---------+---------+---------+

      2410                  2430                  2450
CGACGGGTCTGCCGCGGTTCGATTCCATTCCCAAGCGGCAAGAAGGACGTAGTTAGCTCT
---------+---------+---------+---------+---------+---------+

      2470
GCGTCCCTCGGGATACCA
---------+--------
```

FIG. 3a Cont'd

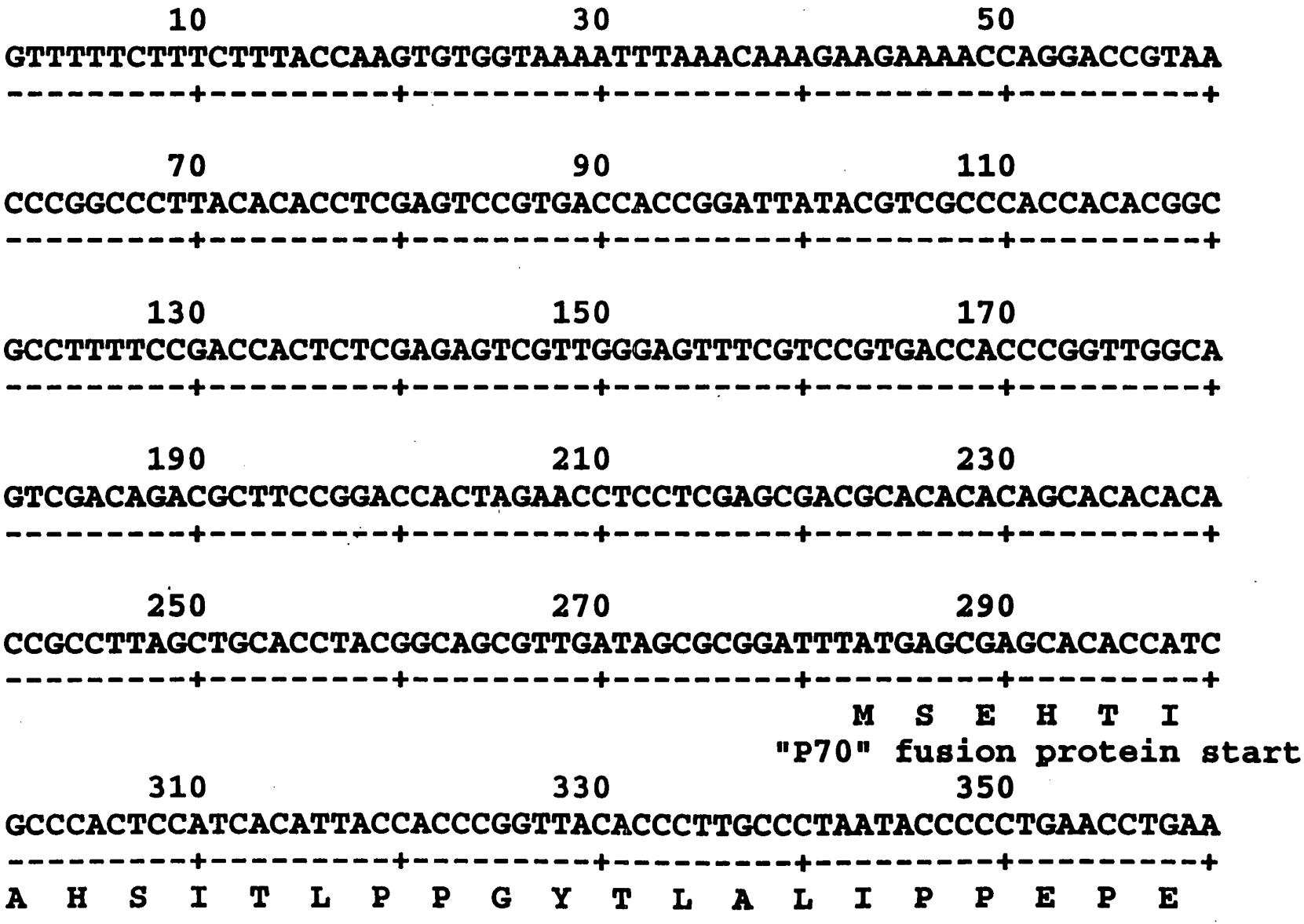

10
30
50
GTTTTTCTTTCTTTACCAAGTGTGGTAAAATTTAAACAAAGAAGAAAACCAGGACCGTAA
70
90
110
CCCGGCCCTTACACACCTCGAGTCCGTGACCACCGGATTATACGTCGCCCACCACACGGC
130
150
170
GCCTTTTCCGACCACTCTCGAGAGTCGTTGGGAGTTTCGTCCGTGACCACCCGGTTGGCA
190
210
230
GTCGACAGACGCTTCCGGACCACTAGAACCTCCTCGAGCGACGCACACACAGCACACACA
250
270
290
CCGCCTTAGCTGCACCTACGGCAGCGTTGATAGCGCGGATTTATGAGCGAGCACACCATC
M S E H T I
"P70" fusion protein start
310
330
350
GCCCACTCCATCACATTACCACCCGGTTACACCCTTGCCCTAATACCCCCTGAACCTGAA
A H S I T L P P G Y T L A L I P P E P E

Fig. 3b

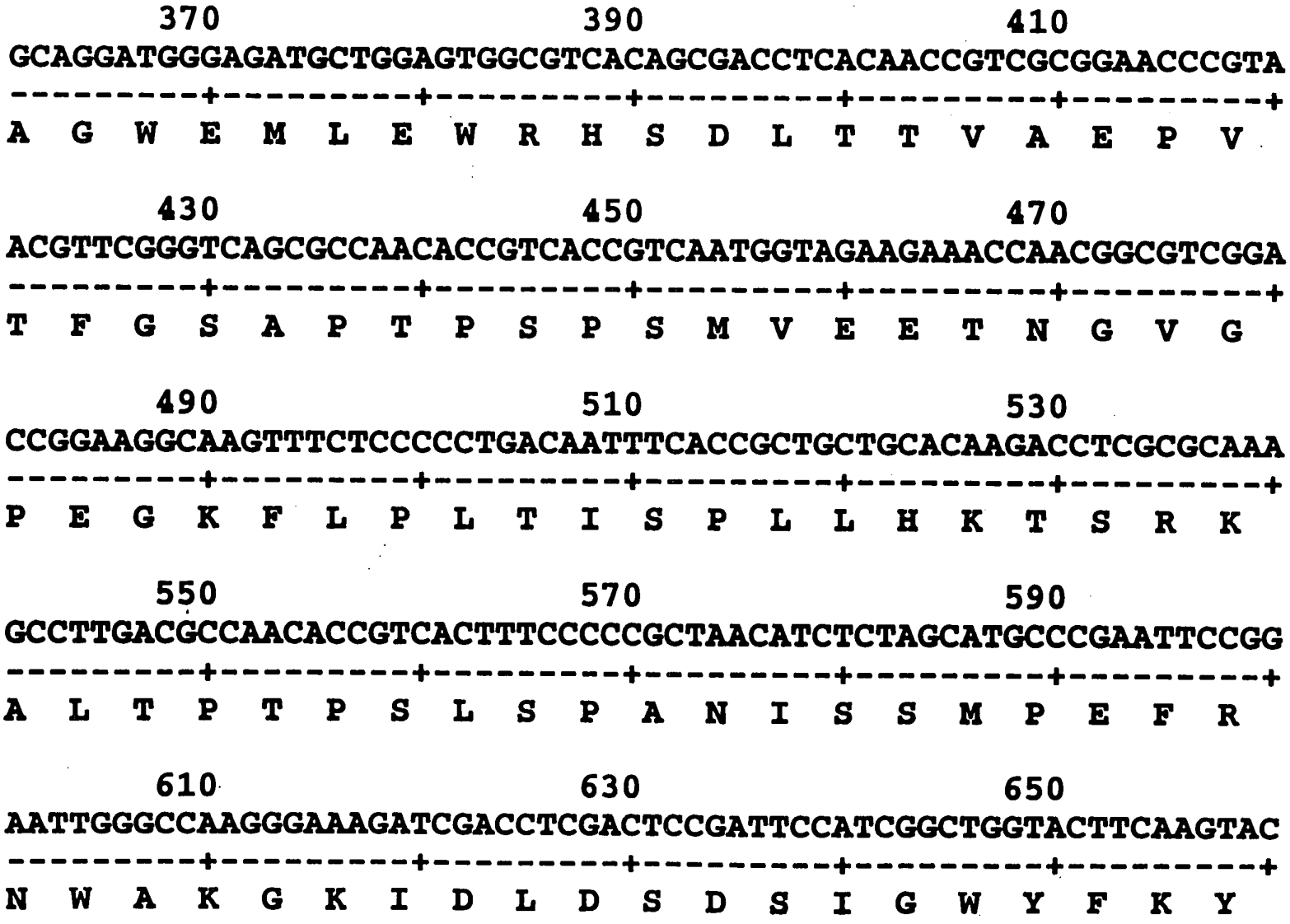

370 390 410
GCAGGATGGGAGATGCTGGAGTGGCGTCACAGCGACCTCACAACCGTCGCGGAACCCGTA
A G W E M L E W R H S D L T T V A E P V
430 450 470
ACGTTCGGGTCAGCGCCAACACCGTCACCGTCAATGGTAGAAGAAACCAACGGCGTCGGA
T F G S A P T P S P S M V E E T N G V G
490 510 530
CCGGAAGGCAAGTTTCTCCCCCTGACAATTTCACCGCTGCTGCACAAGACCTCGCGCAAA
P E G K F L P L T I S P L L H K T S R K
550 570 590
GCCTTGACGCCAACACCGTCACTTTCCCCCGCTAACATCTCTAGCATGCCCGAATTCCGG
A L T P T P S L S P A N I S S M P E F R
610 630 650
AATTGGGCCAAGGGAAAGATCGACCTCGACTCCGATTCCATCGGCTGGTACTTCAAGTAC
N W A K G K I D L D S D S I G W Y F K Y

Fig. 3b (cont'd)

```
       670                 690                 710
CTTGACCCAGCGGGTGCTACAGAGTCTGCGCGCCGTCGGCGAGTACTCGAAGATCCCT
---------+---------+---------+---------+---------+---------+
L  D  P  A  G  A  T  E  S  A  R  A  V  G  E  Y  S  K  I  P

       730                 750                 770
GACGGCCTCGTCAAGTTCTCCGTCGACGCAGAGATAAGAGAGATCTATAACGAGGAGTGC
---------+---------+---------+---------+---------+---------+
D  G  L  V  K  F  S  V  D  A  E  I  R  E  I  Y  N  E  E  C

       790                 810                 830
CCCGTCGTCACTGACGTGTCCGTCCCCCTCGACGGCCGCCAGTGGAGCCTCTCGATTTTC
---------+---------+---------+---------+---------+---------+
P  V  V  T  D  V  S  V  P  L  D  G  R  Q  W  S  L  S  I  F

       850                 870                 890
TCCTTTCCGATGTTCAGAACCGCCTACGTCGCCGTAGCGAACGTCGAGAACAAGGAGATG
---------+---------+---------+---------+---------+---------+
S  F  P  M  F  R  T  A  Y  V  A  V  A  N  V  E  N  K  E  M

       910                 930                 950
TCGCTCGACGTTGTCAACGACCTCATCGAGTGGCTCAACAATCTCGCCGACTGGCGTTAT
---------+---------+---------+---------+---------+---------+
S  L  D  V  V  N  D  L  I  E  W  L  N  N  L  A  D  W  R  Y
```

Fig. 3b(cont'd)

```
   970                 990                1010
GTCGTTGACTCTGAACAGTGGATTAACTTCACCAATGACACCACGTACTACGTCCGCATC
---------+---------+---------+---------+---------+---------+
V  V  D  S  E  Q  W  I  N  F  T  N  D  T  T  Y  Y  V  R  I

  1030                1050                1070
CGCGTTCTACGTCCAACCTACGACGTTCCAGACCCCACAGAGGGCCTTGTTCGCACAGTC
---------+---------+---------+---------+---------+---------+
R  V  L  R  P  T  Y  D  V  P  D  P  T  E  G  L  V  R  T  V

  1090                1110                1130
TCAGACTACCGCCTCACTTATAAGGCGATAACATGTGAAGCCAACATGCCAACACTCGTC
---------+---------+---------+---------+---------+---------+
S  D  Y  R  L  T  Y  K  A  I  T  C  E  A  N  M  P  T  L  V

  1150                1170                1190
GACCAAGGCTTTTGGATCGGCGGCCAGTACGCTCTCACCCCGACTAGCCTACCGCAGTAC
---------+---------+---------+---------+---------+---------+
D  Q  G  F  W  I  G  G  Q  Y  A  L  T  P  T  S  L  P  Q  Y

  1210                1230                1250
GACGTCAGCGAGGCCTACGCTCTGCACACTTTGACCTTCGCCAGACCATCCAGCGCCGCT
---------+---------+---------+---------+---------+---------+
D  V  S  E  A  Y  A  L  H  T  L  T  F  A  R  P  S  S  A  A
```

Fig. 3b (cont'd)

```
         1270                1290                1310
GCACTCGCGTTTGTGTGGGCAGGTTTGCCACAGGGTGGCACTGCGCCTGCAGGCACTCCA
---------+---------+---------+---------+---------+---------+
A  L  A  F  V  W  A  G  L  P  Q  G  G  T  A  P  A  G  T  P

         1330                1350                1370
GCCTGGGAGCAGGCATCCTCGGGTGGCTACCTCACCTGGCGCCACAACGGTACTACTTTC
---------+---------+---------+---------+---------+---------+
A  W  E  Q  A  S  S  G  G  Y  L  T  W  R  H  N  G  T  T  F

         1390                1410                1430
CCAGCTGGCTCCGTTAGCTACGTTCTCCCTGAGGGTTTCGCCCTTGAGCGCTACGACCCG
---------+---------+---------+---------+---------+---------+
P  A  G  S  V  S  Y  V  L  P  E  G  F  A  L  E  R  Y  D  P

         1450                1470                1490
AACGACGGCTCTTGGACCGACTTCGCTTCCGCAGGAGACACCGTCACTTTCCGGCAGGTC
---------+---------+---------+---------+---------+---------+
N  D  G  S  W  T  D  F  A  S  A  G  D  T  V  T  F  R  Q  V

         1510                1530                1550
GCCGTCGACGAGGTCGTTGTGACCAACAACCCCGCCGGCGGCGGCAGCGCCCCCACCTTC
---------+---------+---------+---------+---------+---------+
A  V  D  E  V  V  V  T  N  N  P  A  G  G  G  S  A  P  T  F
```

Fig. 3b (cont'd)

```
        1570                1590                1610
ACCGTGAGAGTGCCCCCTTCAAACGCTTACACCAACACCGTGTTTAGGAACACGCTCTTA
---------+---------+---------+---------+---------+---------+
T  V  R  V  P  P  S  N  A  Y  T  N  T  V  F  R  N  T  L  L

        1630                1650                1670
GAGACTCGACCCTCCTCTCGTAGGCTCGAACTCCCTATGCCACCTGCTGACTTTGGACAG
---------+---------+---------+---------+---------+---------+
E  T  R  P  S  S  R  R  L  E  L  P  M  P  P  A  D  F  G  Q

        1690                1710                1730
ACGGTCGCCAACAACCCGAAGATCGAGCAGTCGCTTCTTAAAGAAACACTTGGCTGCTAT
---------+---------+---------+---------+---------+---------+
T  V  A  N  N  P  K  I  E  Q  S  L  L  K  E  T  L  G  C  Y

        1750                1770                1790
TTGGTCCACTCCAAAATGCGAAACCCCGTTTTCCAGCTCACGCCAGCCAGCTCCTTTGGC
---------+---------+---------+---------+---------+---------+
L  V  H  S  K  M  R  N  P  V  F  Q  L  T  P  A  S  S  F  G

        1810                1830                1850
GCCGTTTCCTTCAACAATCCGGGTTATGAGCGCACACGCGACCTCCCGGACTACACTGGC
---------+---------+---------+---------+---------+---------+
A  V  S  F  N  N  P  G  Y  E  R  T  R  D  L  P  D  Y  T  G
```

Fig. 3b (cont'd)

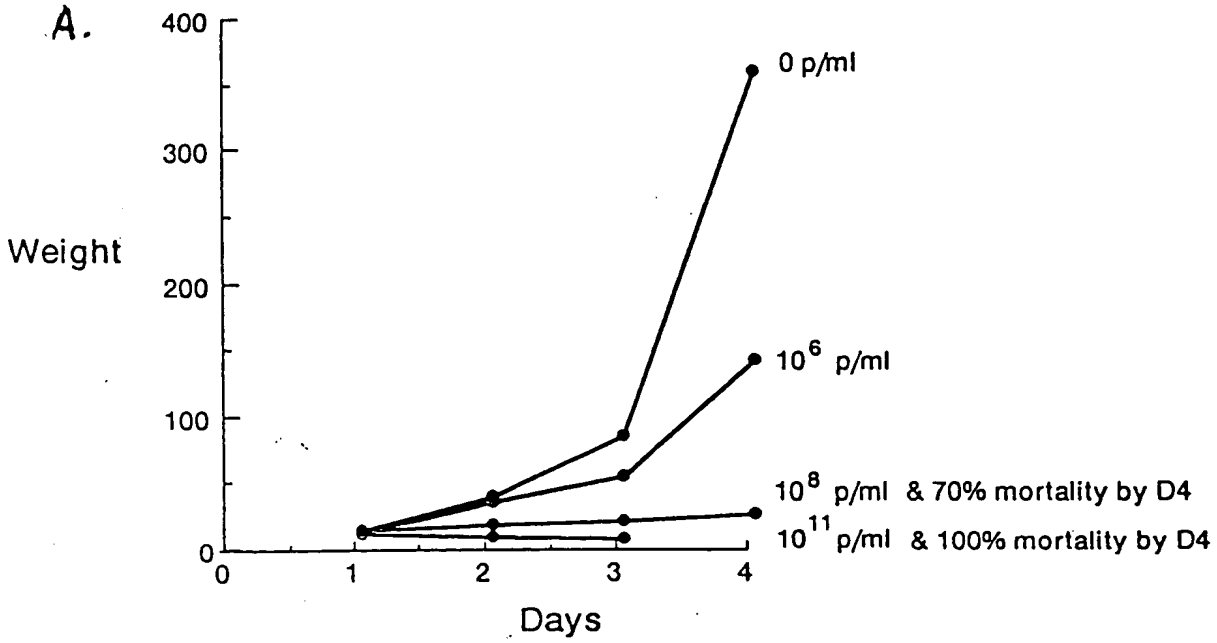
```
      1870                  1890                  1910
ATCCGTGACTCATTCGACCAGAACATGTCCACCGCTGTGGCCCACTTCCGCTCACTCTCC
--------+---------+---------+---------+---------+---------+
I  R  D  S  F  D  Q  N  M  S  T  A  V  A  H  F  R  S  L  S

      1930                  1950                  1970
CACTCCTGCAGTATCGTCACTAAGACCTACCAGGGTTGGGAAGGCGTCACGAACGTCAAC
--------+---------+---------+---------+---------+---------+
H  S  C  S  I  V  T  K  T  Y  Q  G  W  E  G  V  T  N  V  N

      1990                  2010                  2030
ACGCCTTTCGGCCAATTCGCGCACGCGGGCCTCCTCAAGAATGAGGAGATCCTCTGCCTC
--------+---------+---------+---------+---------+---------+
T  P  F  G  Q  F  A  H  A  G  L  L  K  N  E  E  I  L  C  L

      2050                  2070                  2090
GCCGACGACCTGGCCACCCGTCTCACAGGTGTCTACCCCGCCACTGACAACTTCGCGGCC
--------+---------+---------+---------+---------+---------+
A  D  D  L  A  T  R  L  T  G  V  Y  P  A  T  D  N  F  A  A

      2110                  2130                  2150
GCCGTTTCTGCCTTCGCCGCGAACATGCTGTCCTCCGTGCTGAAGTCGGAGGCAACGTCC
--------+---------+---------+---------+---------+---------+
A  V  S  A  F  A  A  N  M  L  S  S  V  L  K  S  E  A  T  S
```

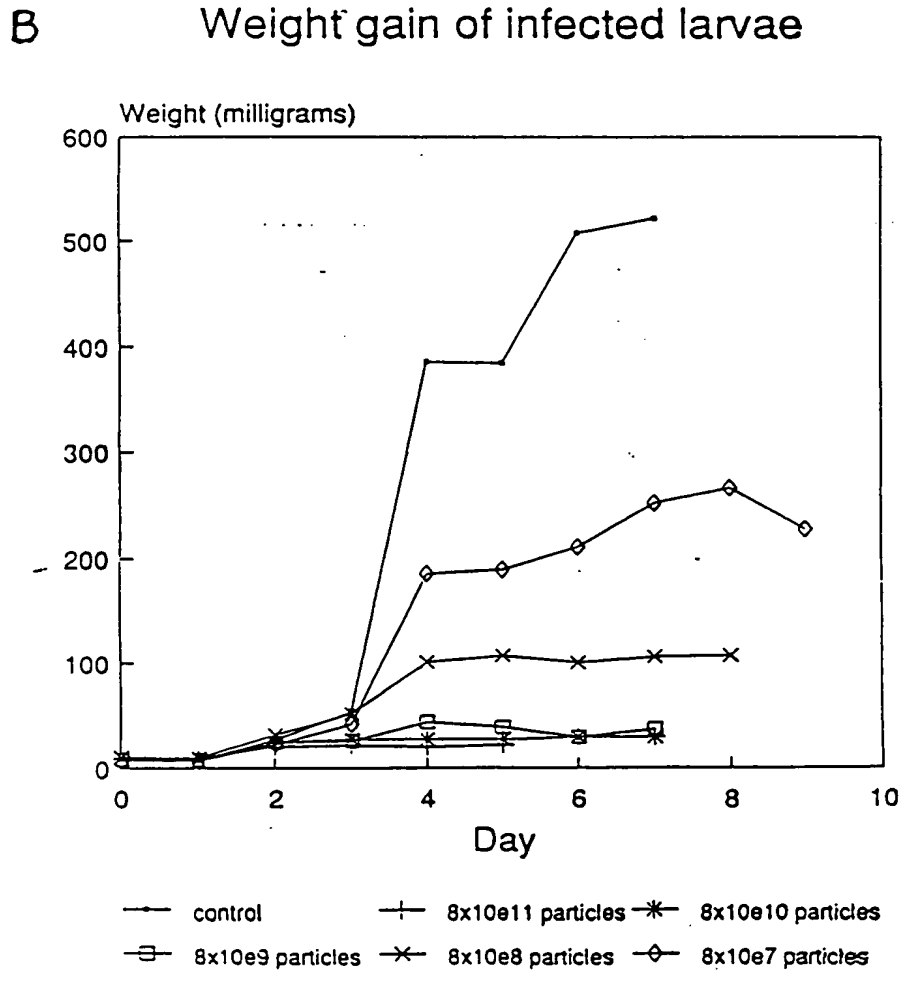
Fig. 3b (cont'd)

```
      2170                    2190                    2210
TCCATCATCAAGTCCGTTGGCGAGACTGCCGTCGGCGCGGCTCAGTCCGGCCTCGCGAAG
--------+---------+---------+---------+---------+---------+---------+
S  I  I  K  S  V  G  E  T  A  V  G  A  A  Q  S  G  L  A  K

      2230                    2250                    2270
CTACCCGGACTGCTAATGAGTGTACCAGGGAAGATTGCCGCGCGTGTCCGCGCGCGCCGA
--------+---------+---------+---------+---------+---------+---------+
L  P  G  L  L  M  S  V  P  G  K  I  A  A  R  V  R  A  R  R

      2290                    2310                    2330
GCGCGCCGCCGCGCCGCTCGTGCCAATTAGTTTGCTCGCTCCTGTTTCGCCGTTTCGTAA
--------+---------+---------+---------+---------+---------+---------+
A  R  R  R  A  A  R  A  N  *

      2350                    2370                    2390
AACGGCGTGGTCCCGCACATTACGCGTACCCTAAAGACTCTGGTGAGTCCCCGTCGTTAC
--------+---------+---------+---------+---------+---------+---------+

      2410                    2430                    2450
ACGACGGGTCTGCCGCGGTTCGATTCCATTCCCAAGCGGCAAGAAGGACGTAGTTAGCTC
--------+---------+---------+---------+---------+---------+---------+

      2470
TGCGTCCCTCGGGATACCA
--------+---------
```

Fig. 3b (cont'd)

FIG. 4


A.
Weight
400
300
200
100
0
0
1
2
3
4
Days
0 p/ml
10^6 p/ml
10^8 p/ml & 70% mortality by D4
10^11 p/ml & 100% mortality by D4


B
Weight gain of infected larvae
Weight (milligrams)
600
500
400
300
200
100
0
0
2
4
6
8
10
Day
control
8x10e11 particles
8x10e10 particles
8x10e9 particles
8x10e8 particles
8x10e7 particles

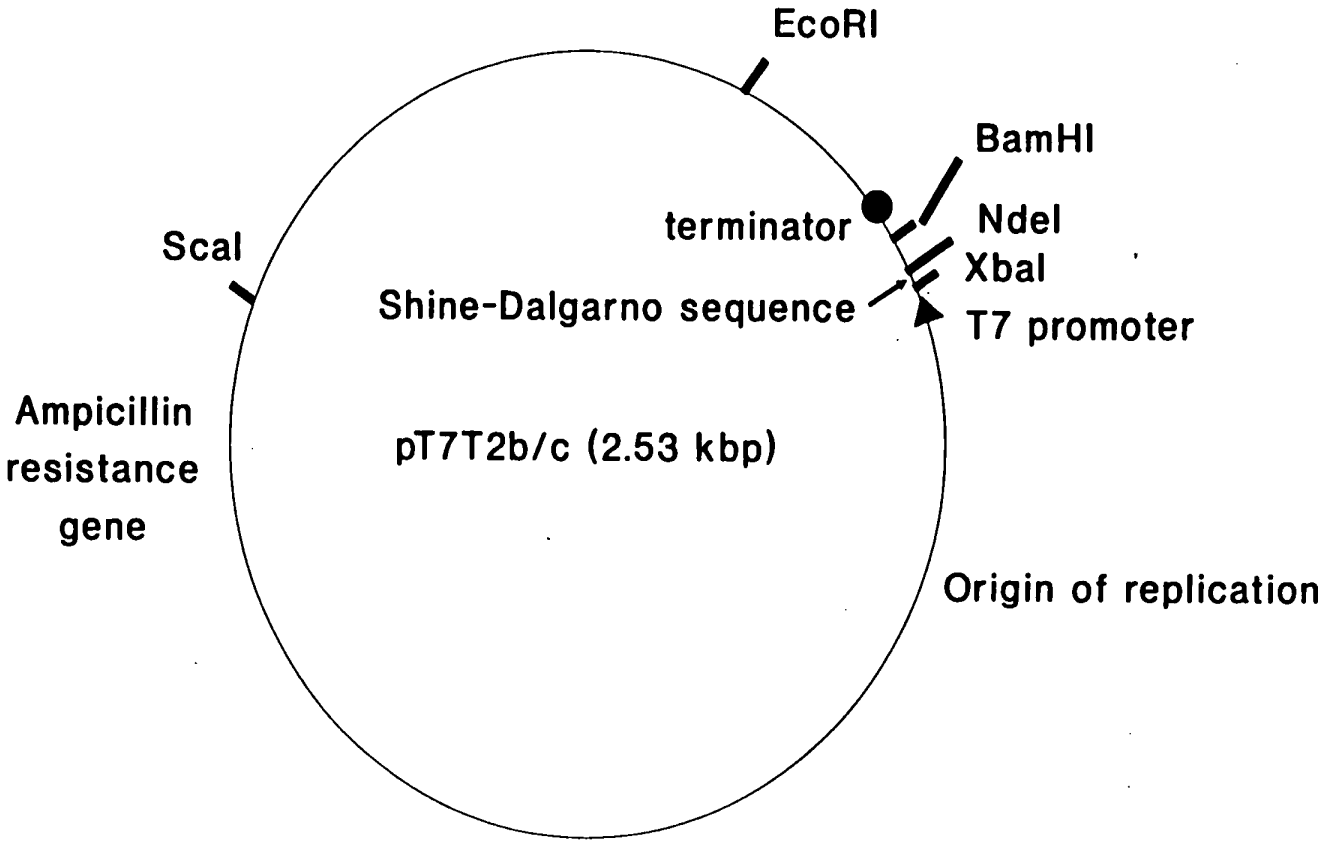


Fig. 5

Proteins encoded by the HaSV genome

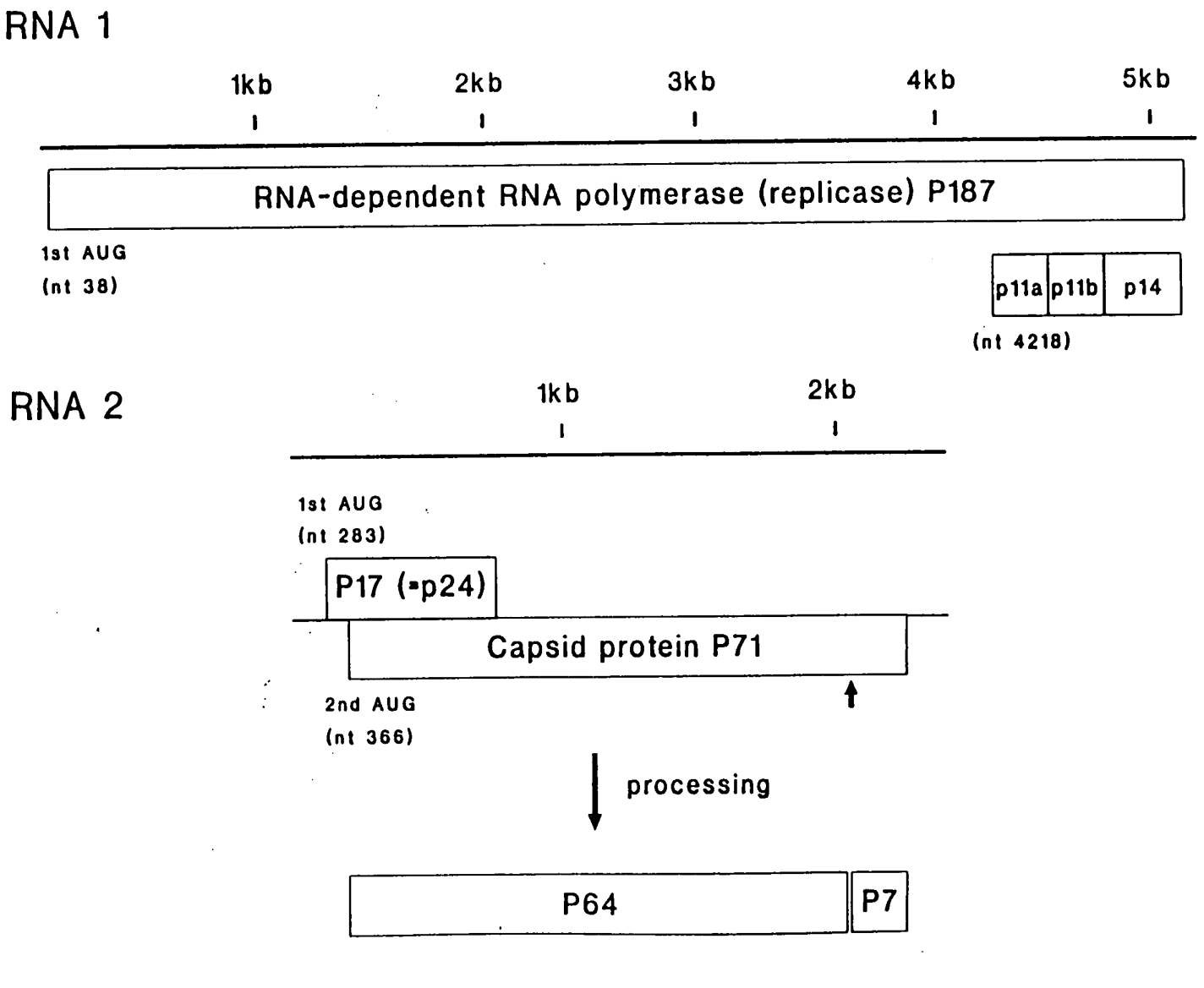


FIG. 6

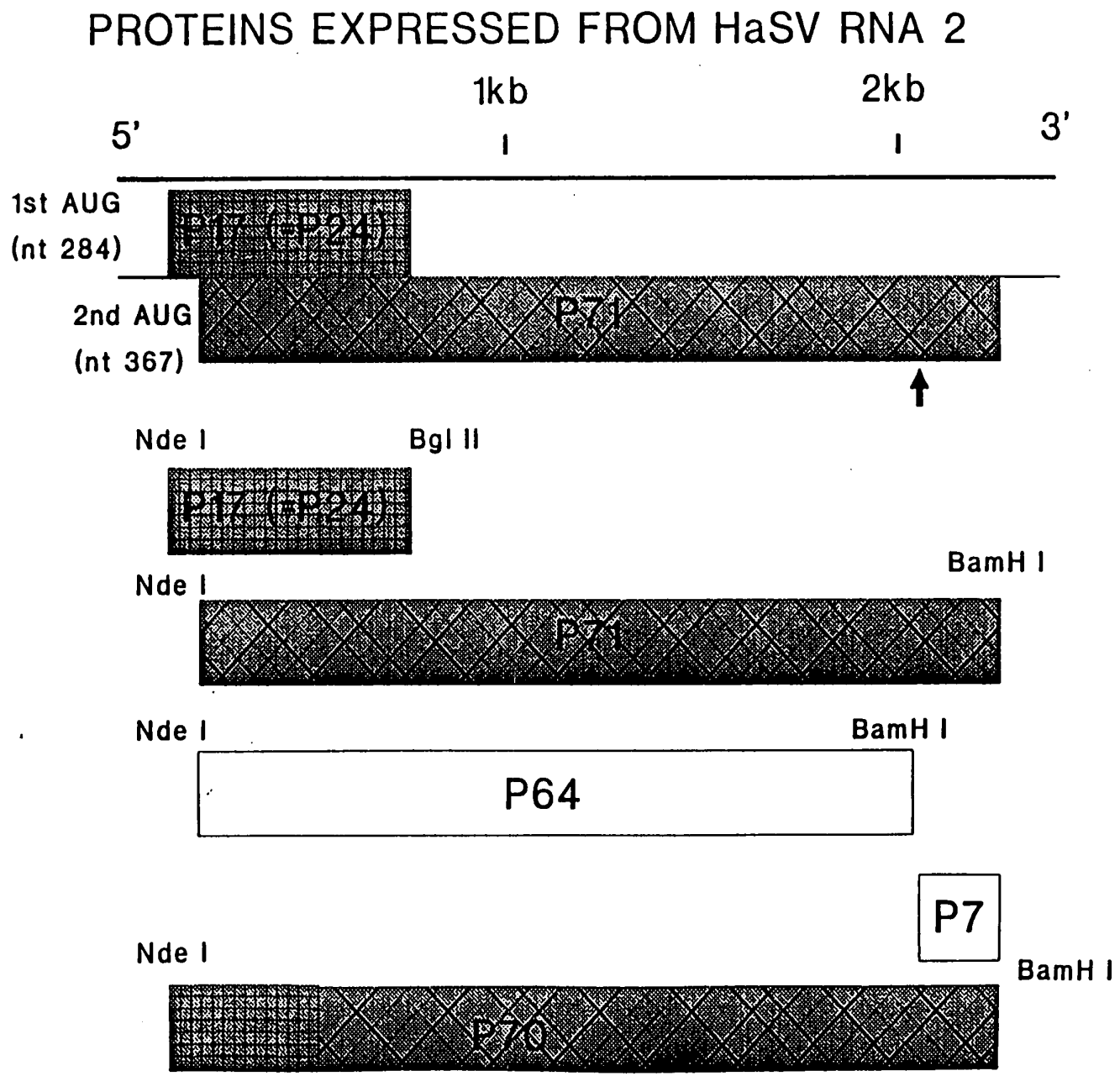
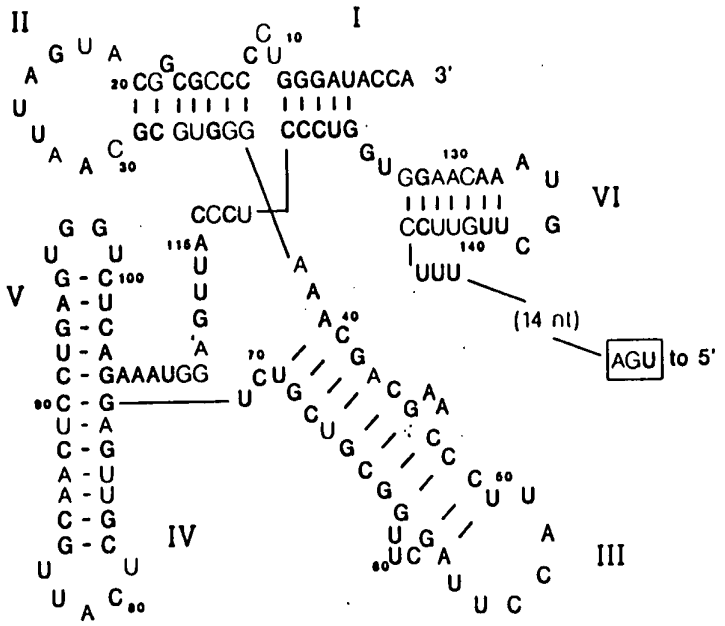


FIG. 7

HaSV RNA 3' - terminal tRNA-like structures

RNA 1



RNA 2

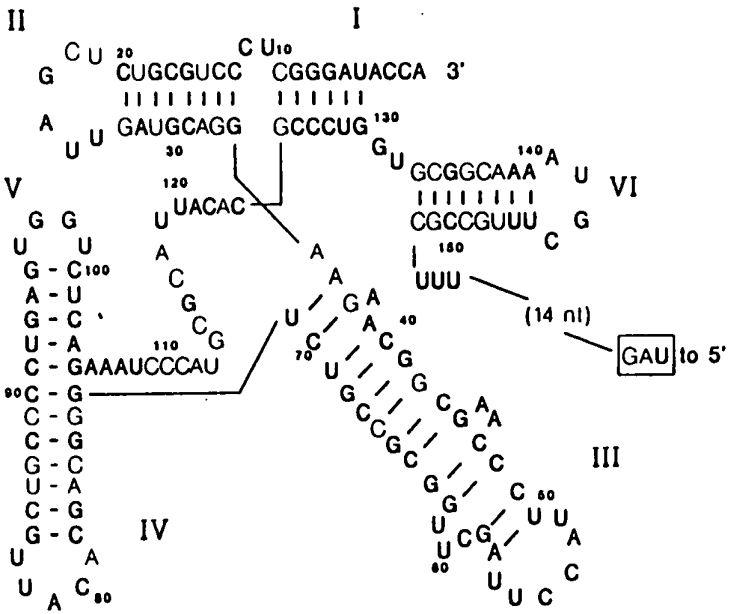


FIG. 8

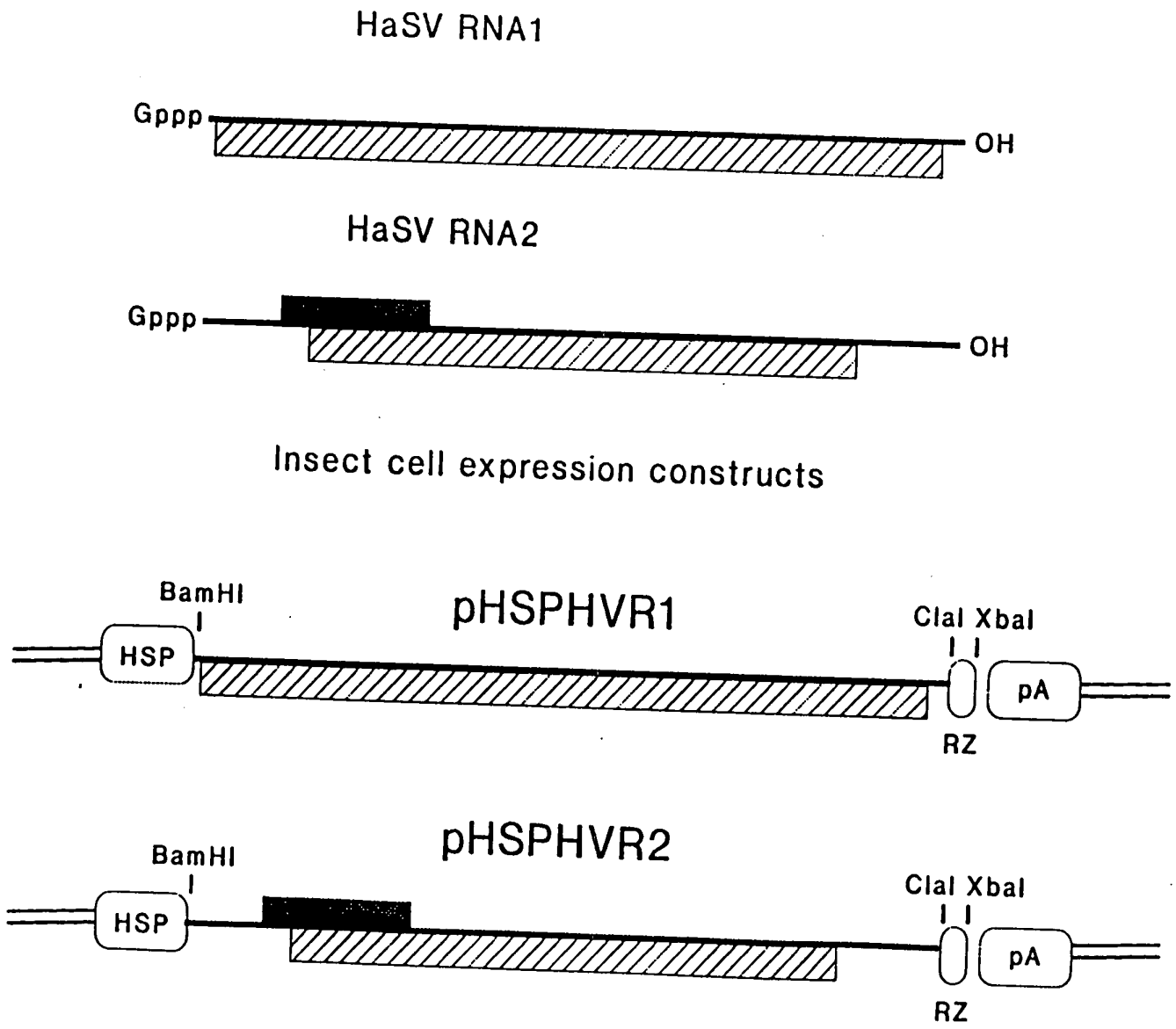
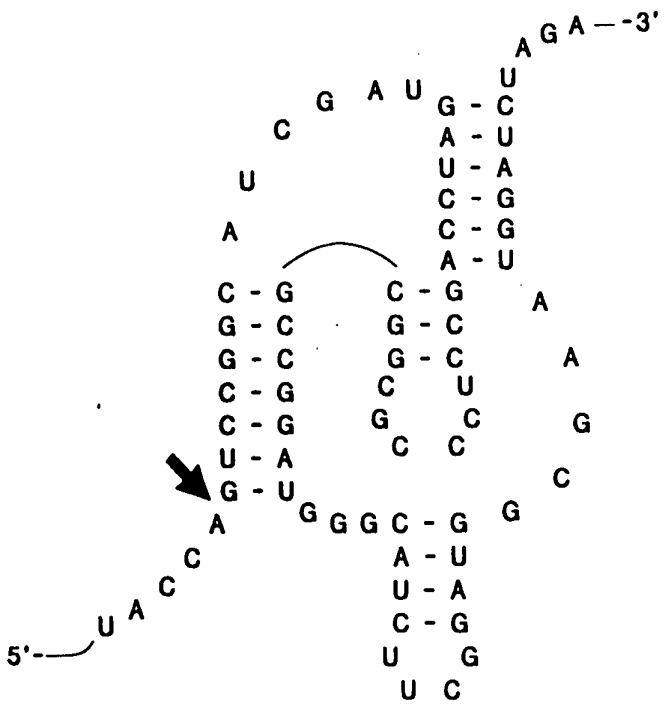


Fig. 9

CIS-ACTING RIBOZYMES FOR HASV 3' ENDS

HEPATITIS DELTA VIRUS



HAIRPIN

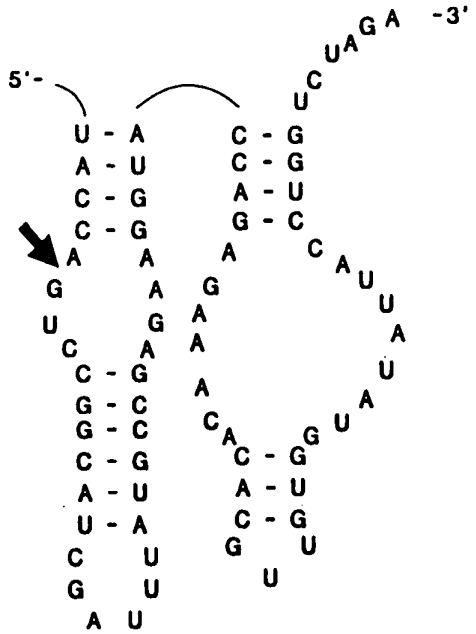
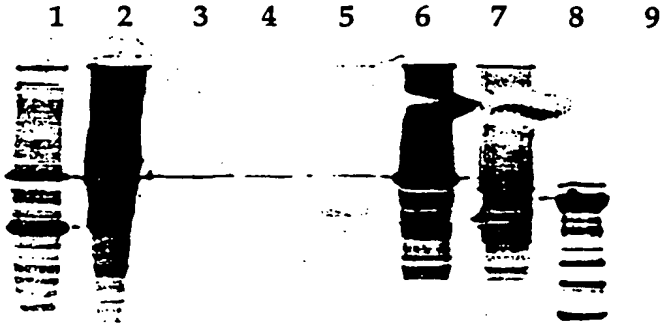


FIG. 10

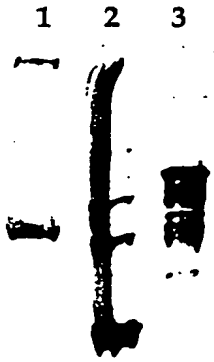
FIG. 11

WESTERN BLOTS OF HaSV CAPSID PROTEIN

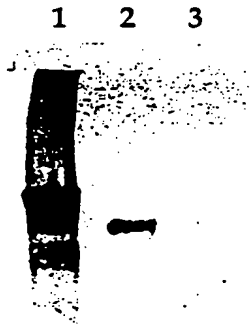
A. HaSV ANTISERUM



B HaSV ANTISERUM



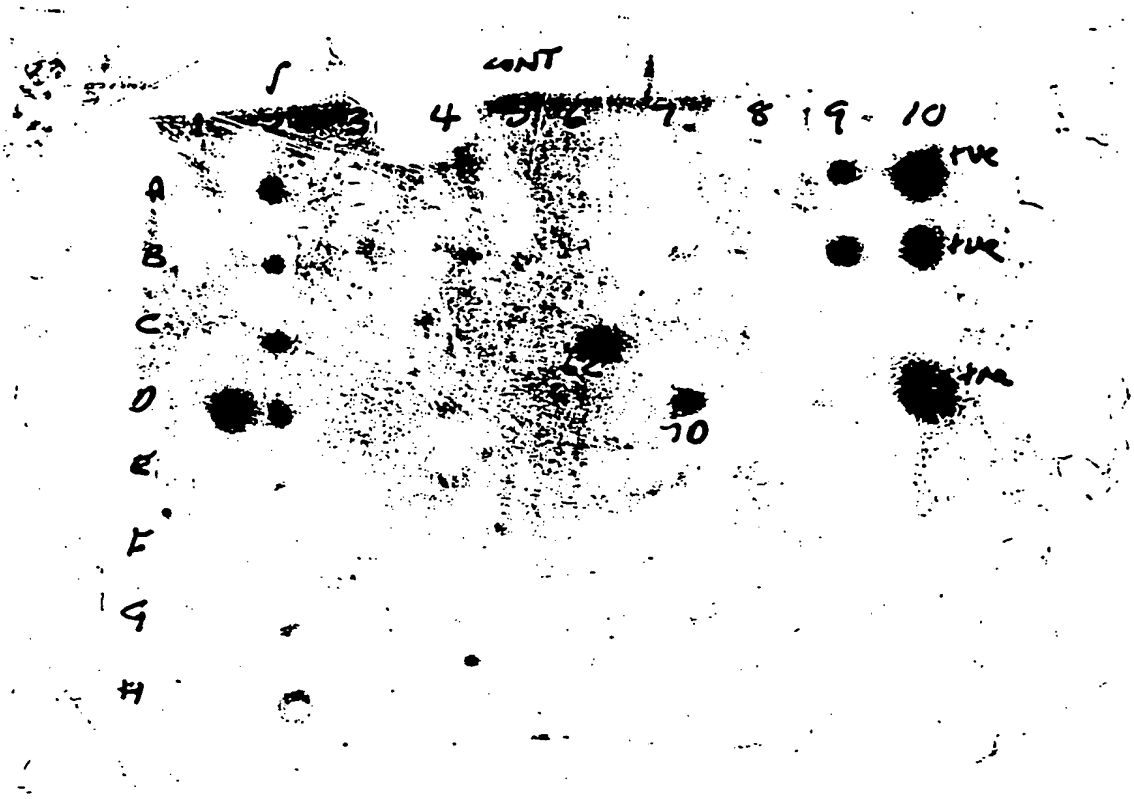
C. Bt ANTISERUM



Bt toxin cfs

FIG. 12

DOT-BLOT DETECTION OF HaSV IN FIELD-COLLECTED HELICOVERPA LARVAE



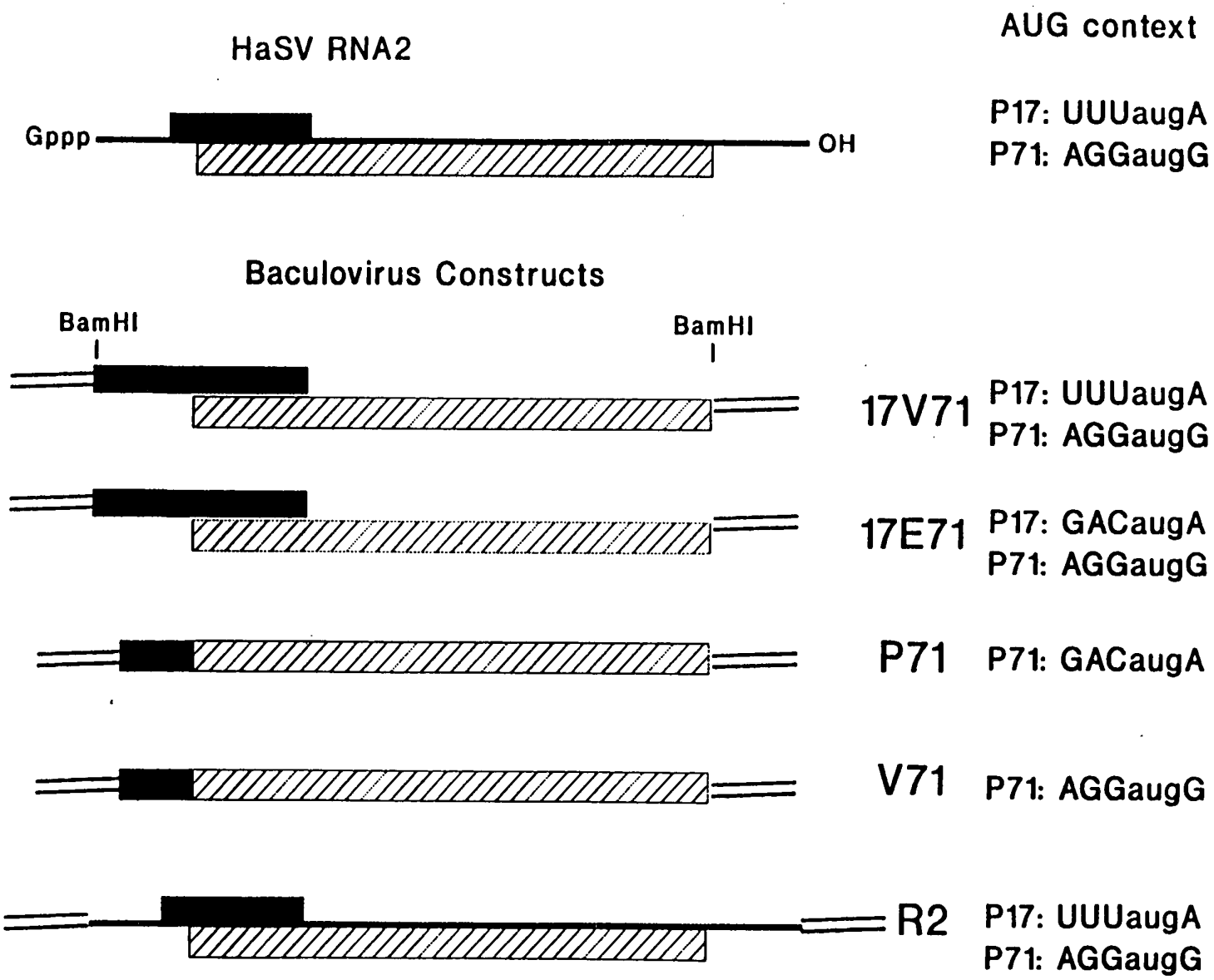


Fig. 13

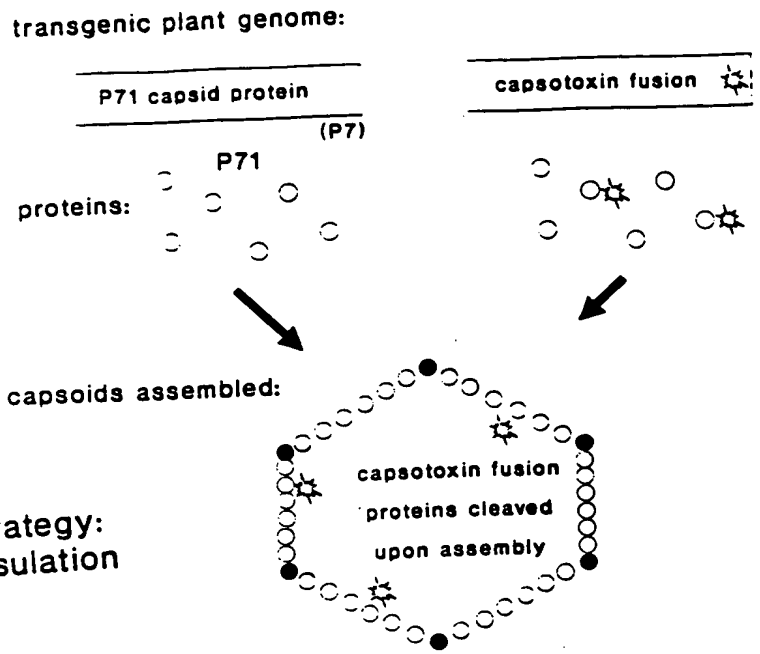
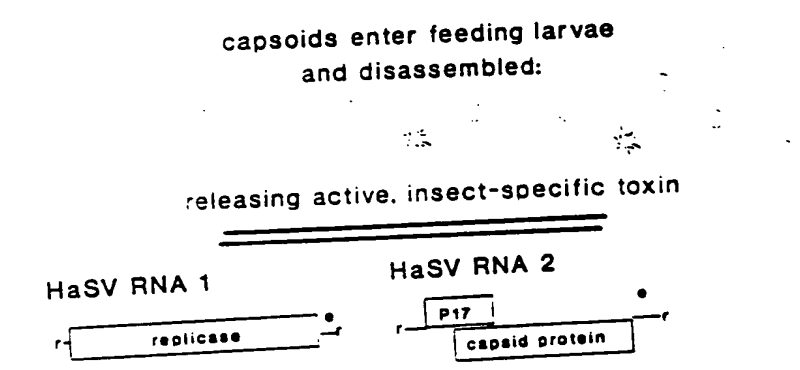


FIG. 14a

Virus capsoid strategy:
capsotoxin encapsulation



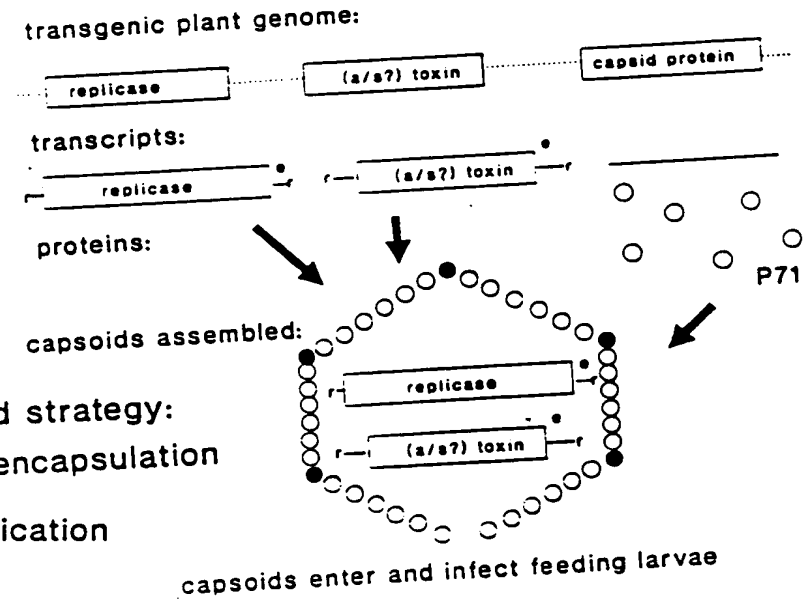


FIG. 14b

Virus capsoid strategy:
toxin message encapsulation
and amplification

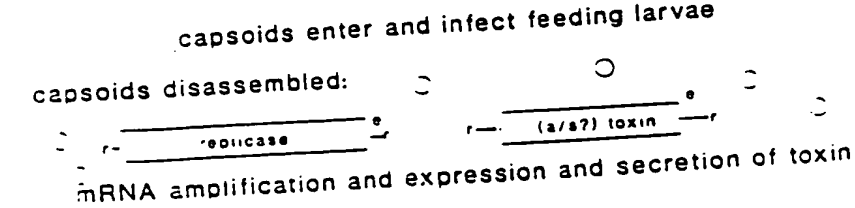


FIG. 14c

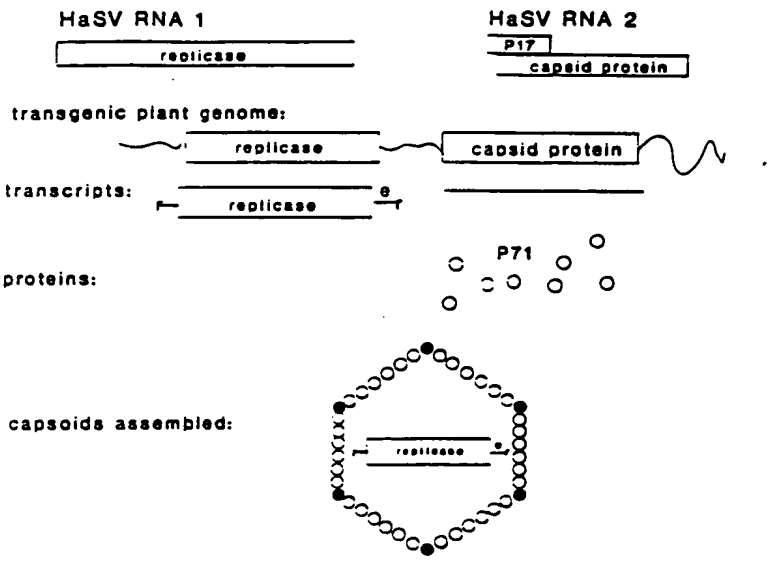
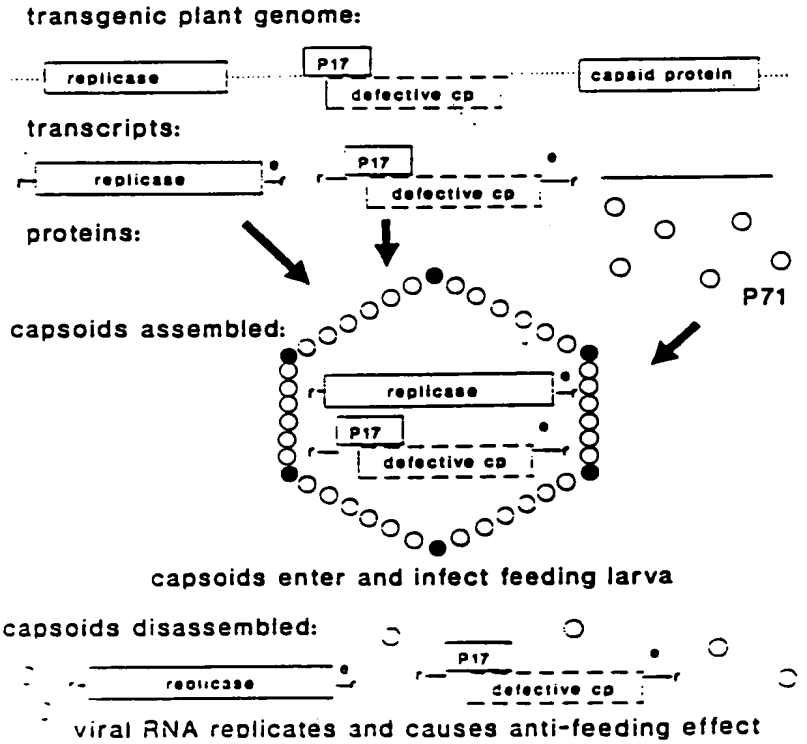
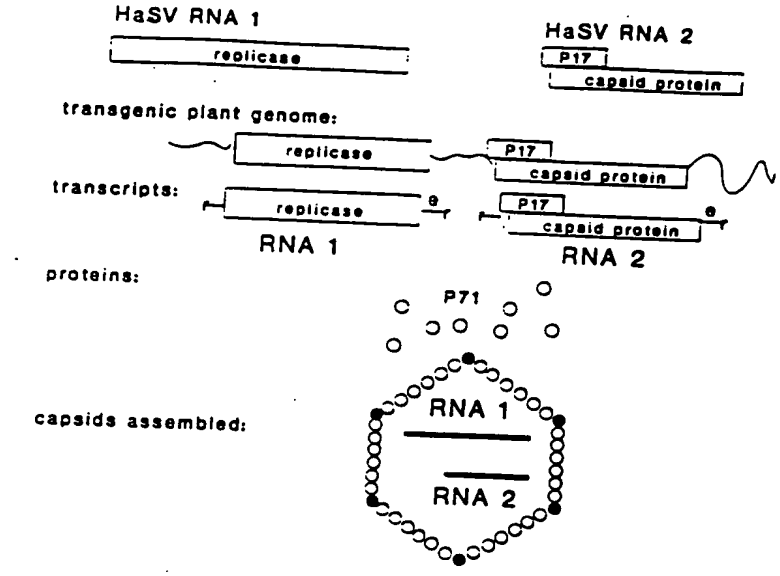


FIG. 14d



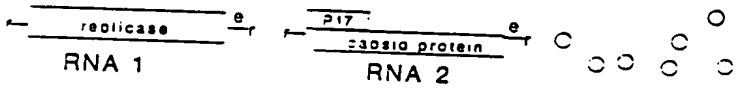
Virus expression in plants:

FIG. 14e



capsids enter and infect feeding larvae

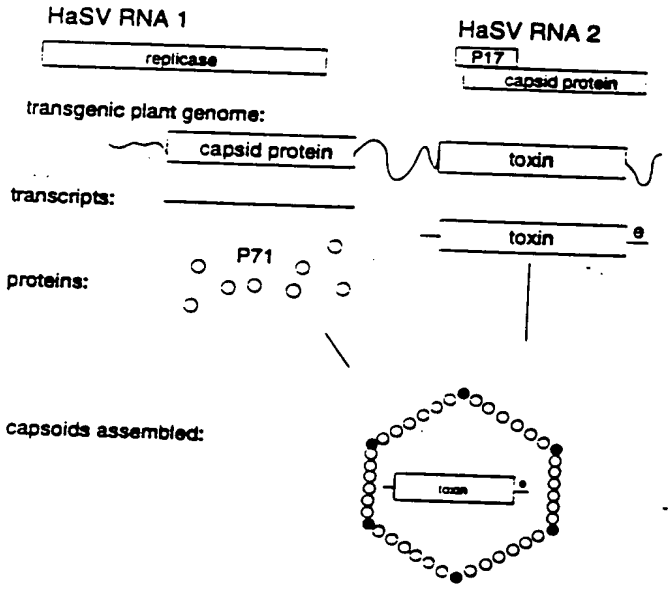
capsids disassembled:



virus replicates and causes anti-feeding effect

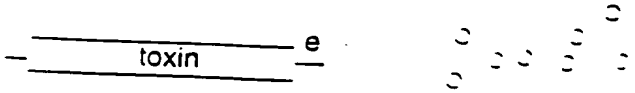
Virus expression in plants: the one-way vector for a toxin

FIG. 14f



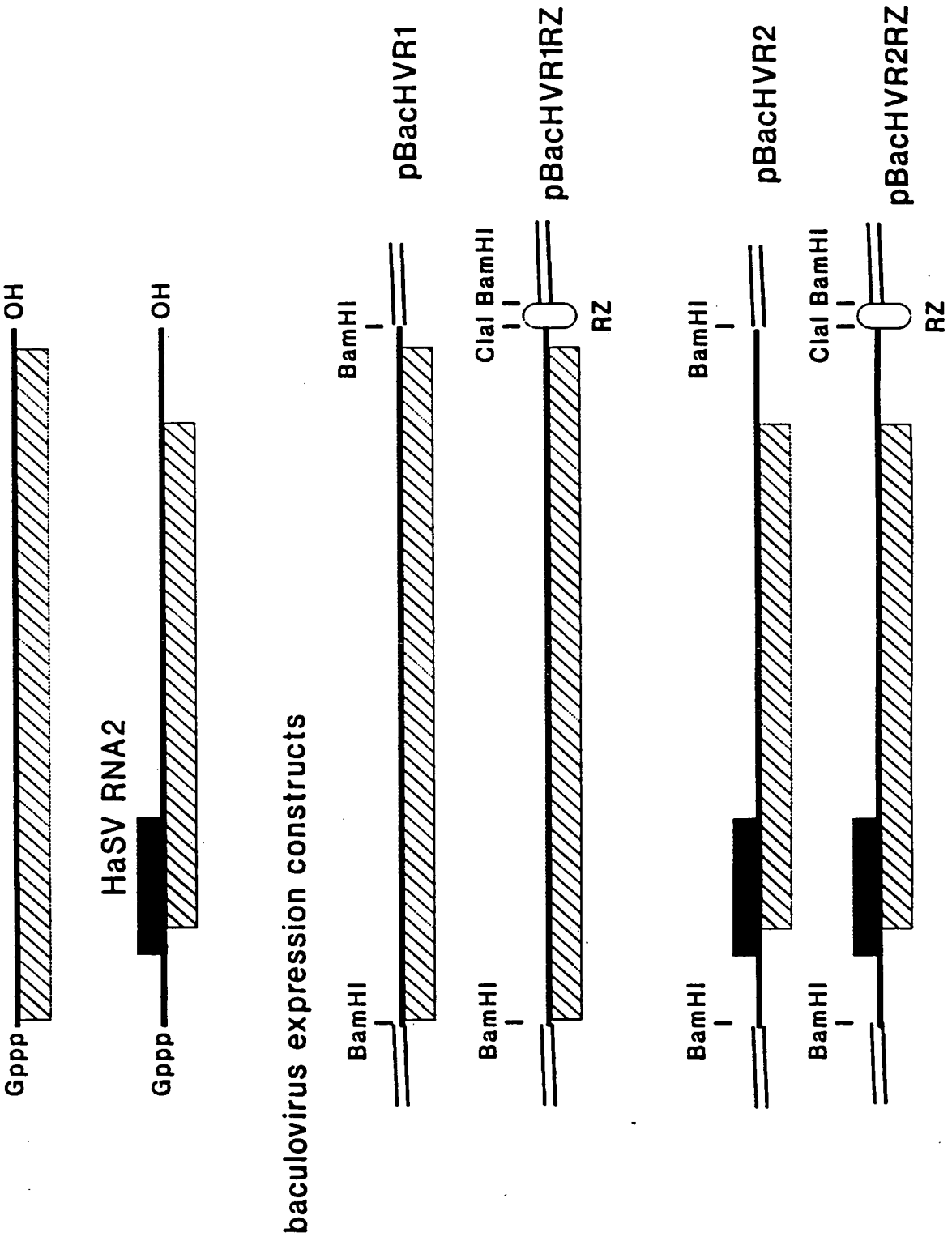
capsoids enter and infect feeding larvae

capsoids disassembled:



toxin expressed and causes larvae to cease feeding

Fig. 15


HaSV RNA1
Gppp
OH
HaSV RNA2
Gppp
OH
baculovirus expression constructs
pBacHVR1
BamHI
BamHI
pBacHVR1RZ
ClaI BamHI
RZ
BamHI
pBacHVR2
BamHI
BamHI
pBacHVR2RZ
ClaI BamHI
RZ
BamHI

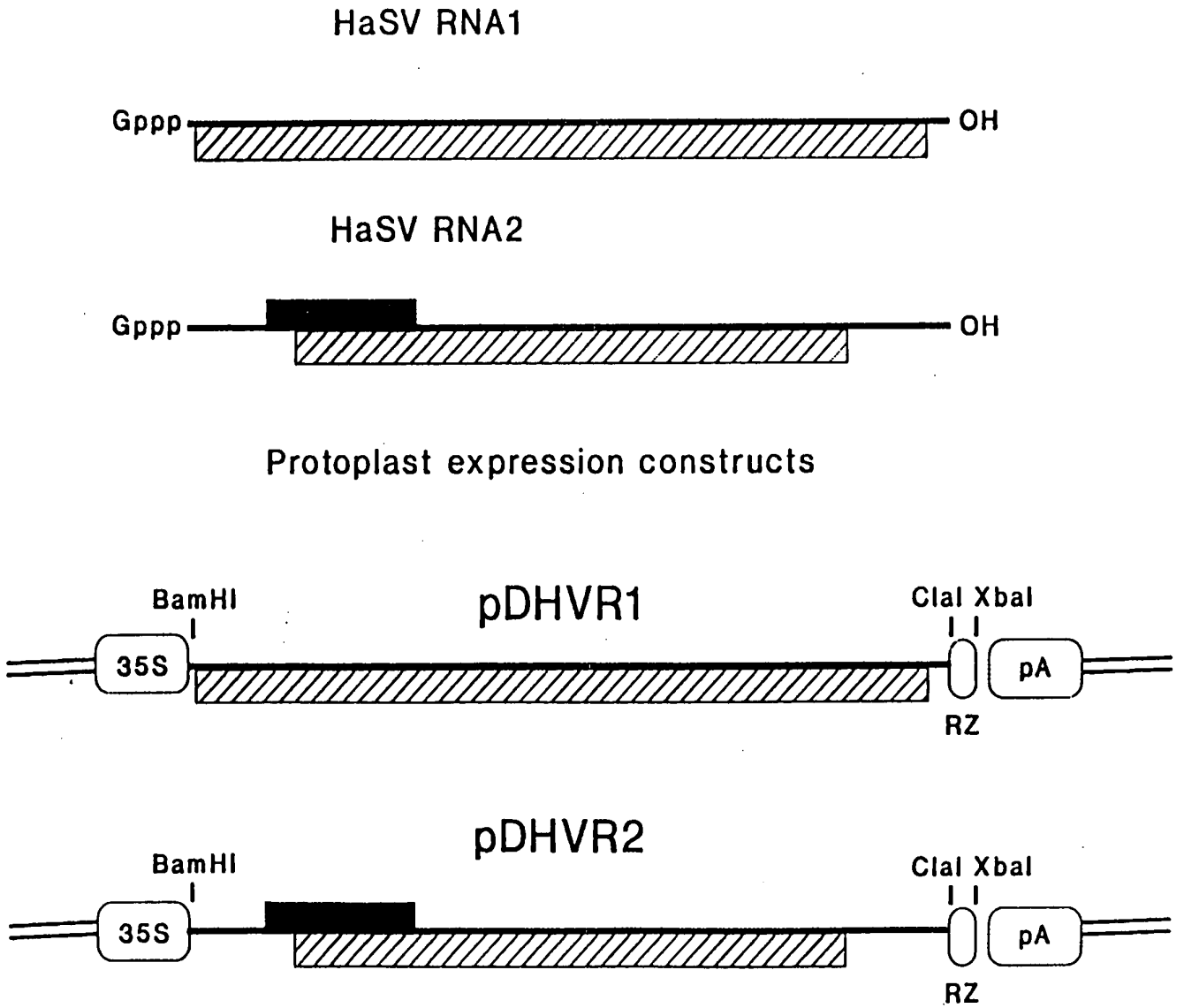


Fig. 16